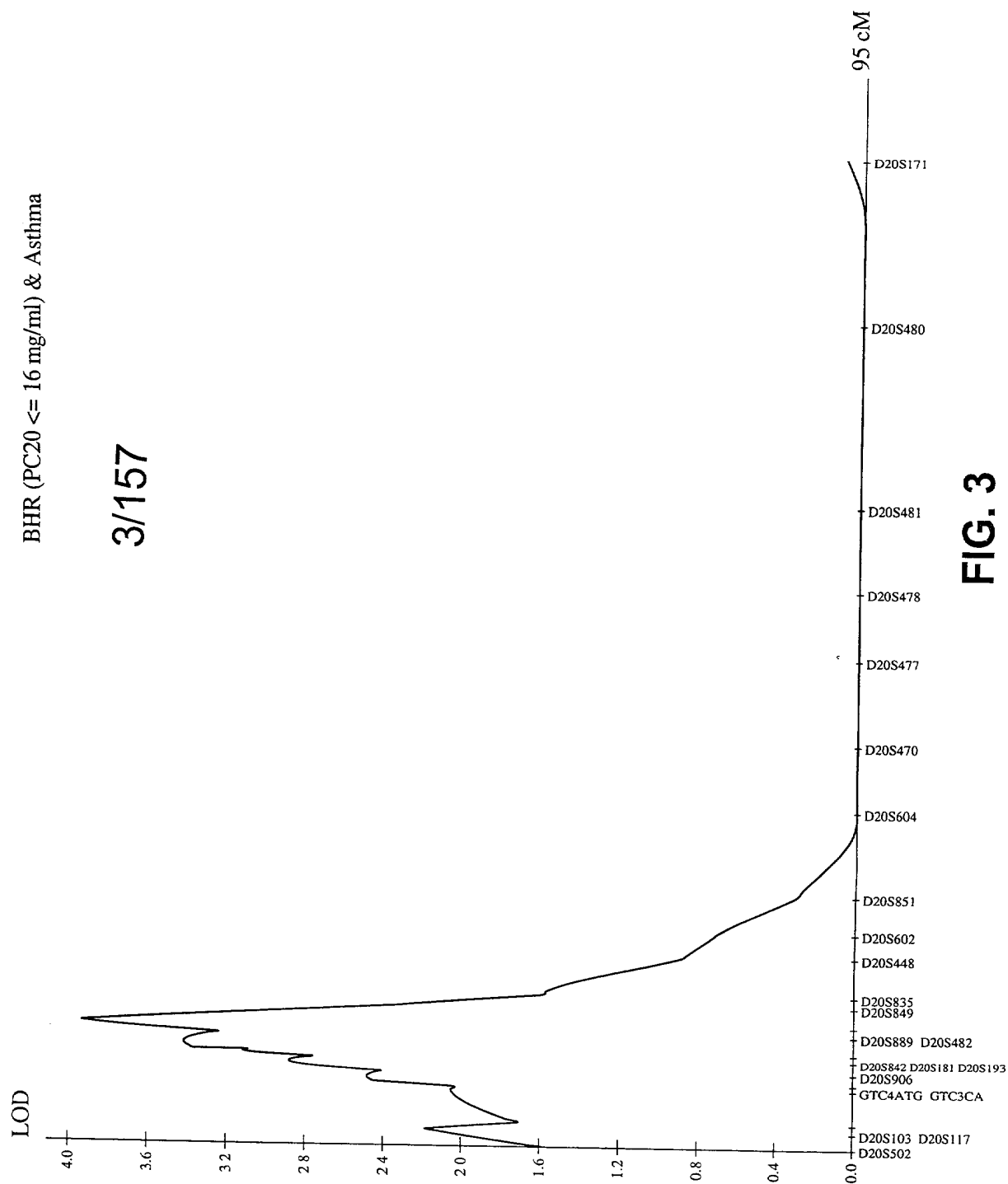


FIG. 2

BHR (PC20 \leq 16 mg/ml) & Asthma

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High Total IgE & Asthma

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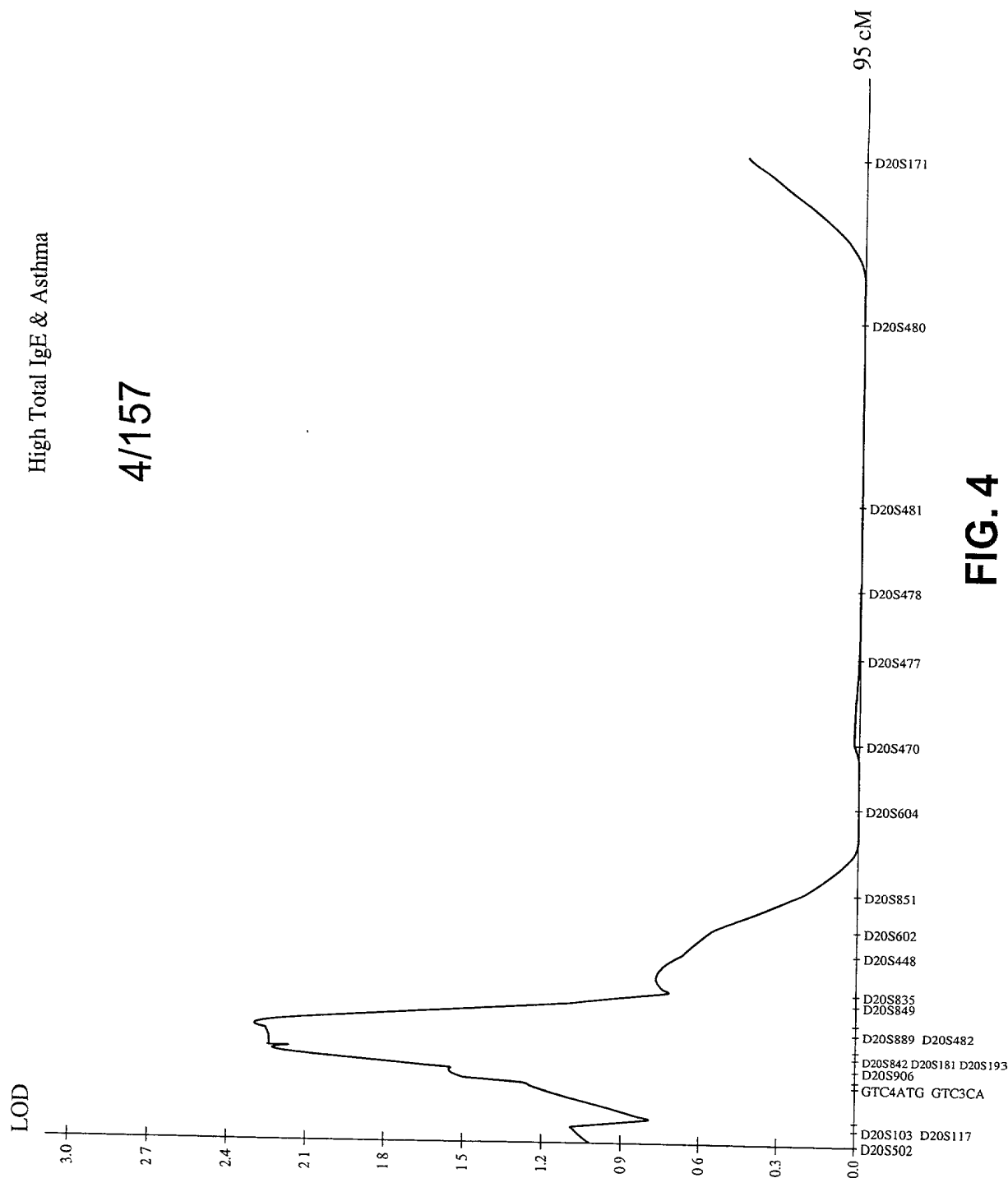


FIG. 4

High Specific IgE & Asthma

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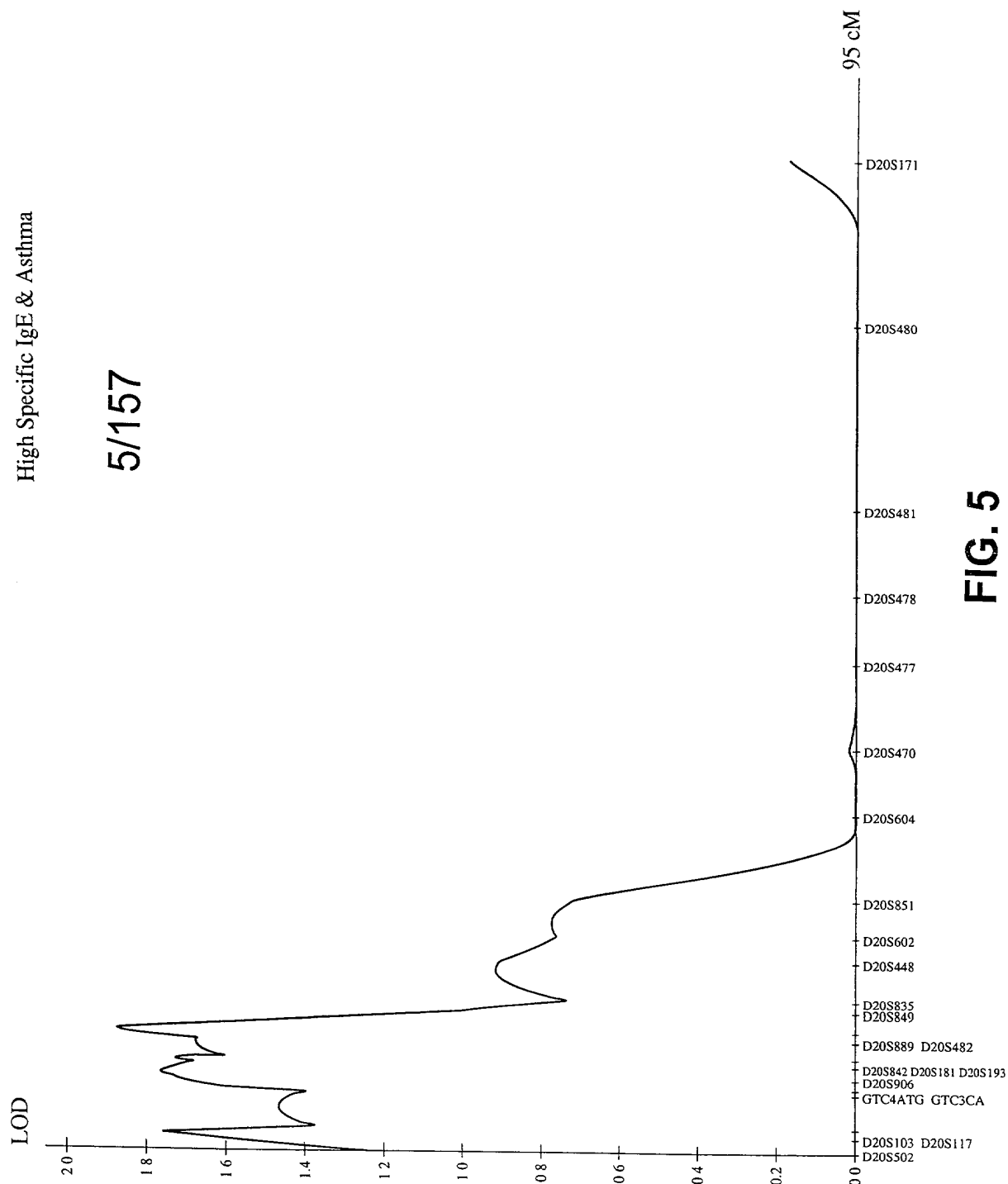


FIG. 5

FIG. 6

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>BAC1098L22 sequence

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

FIG. 7

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FIG. 7

FIG. 7

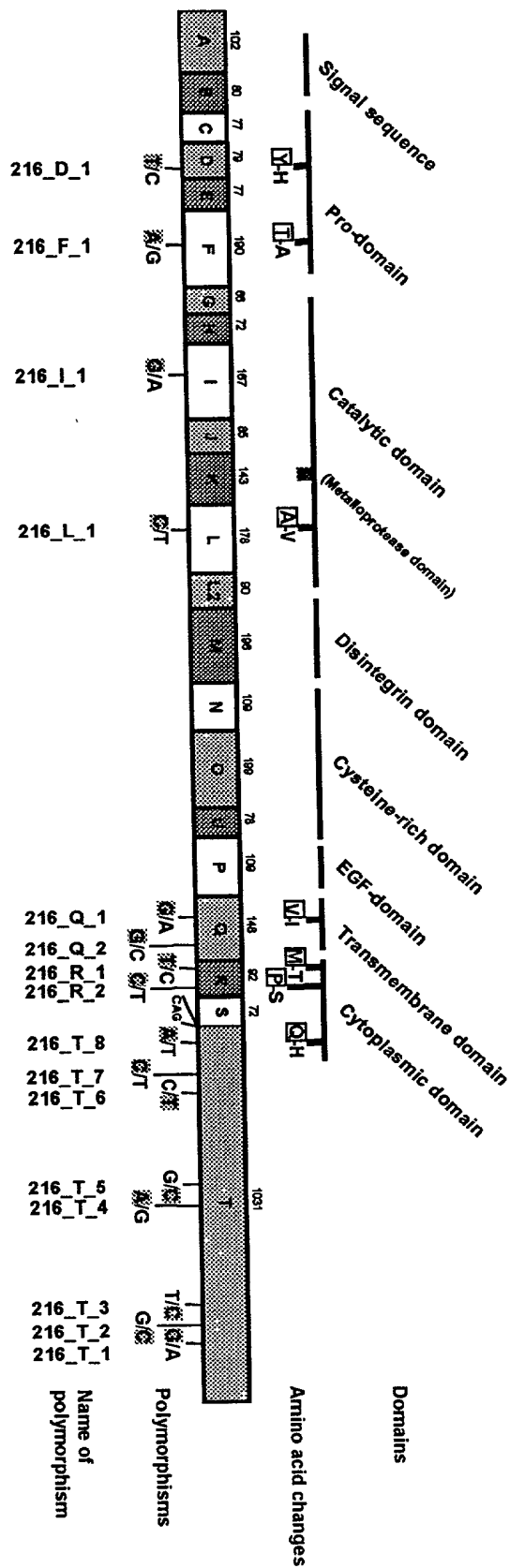


FIG. 8

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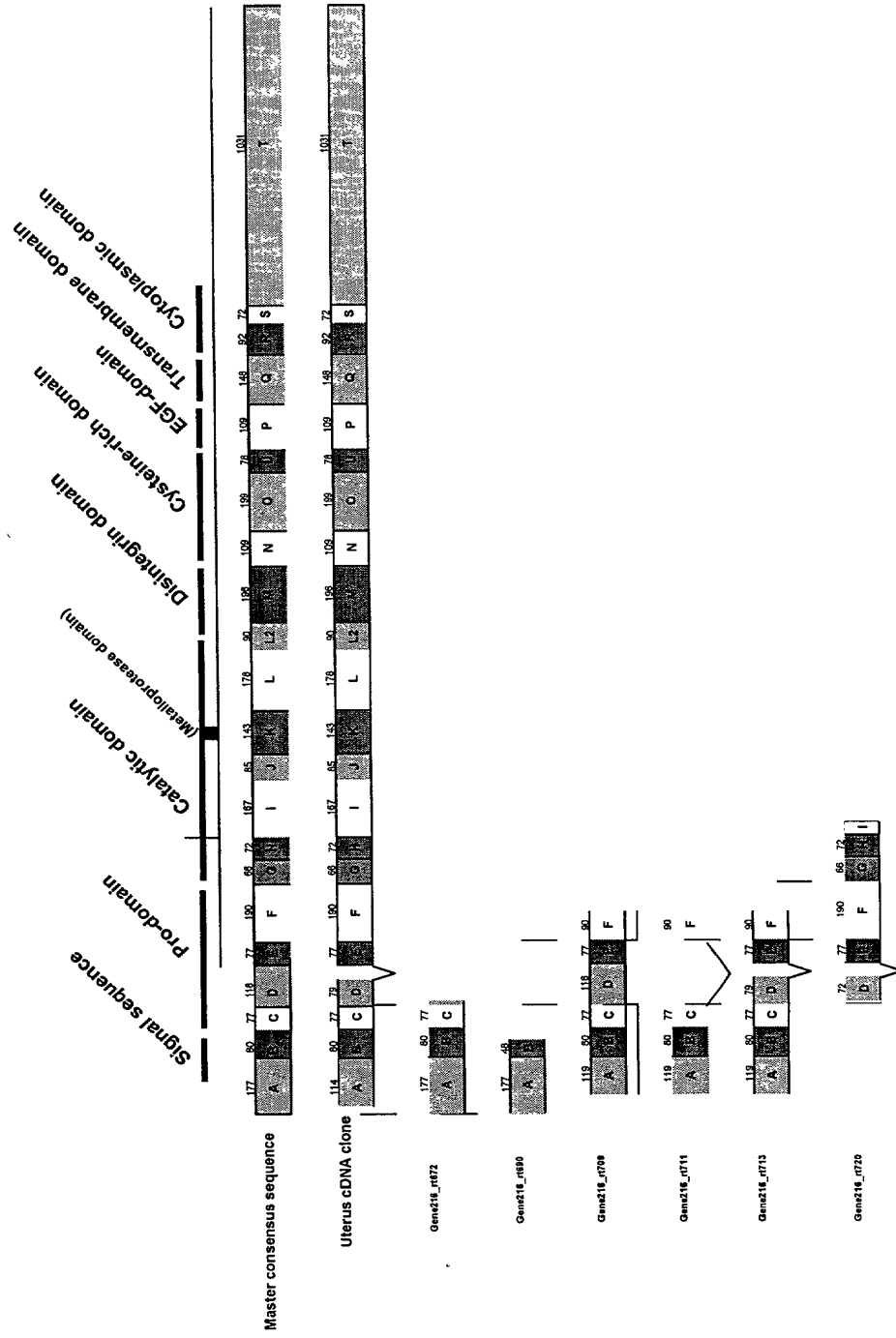
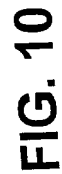
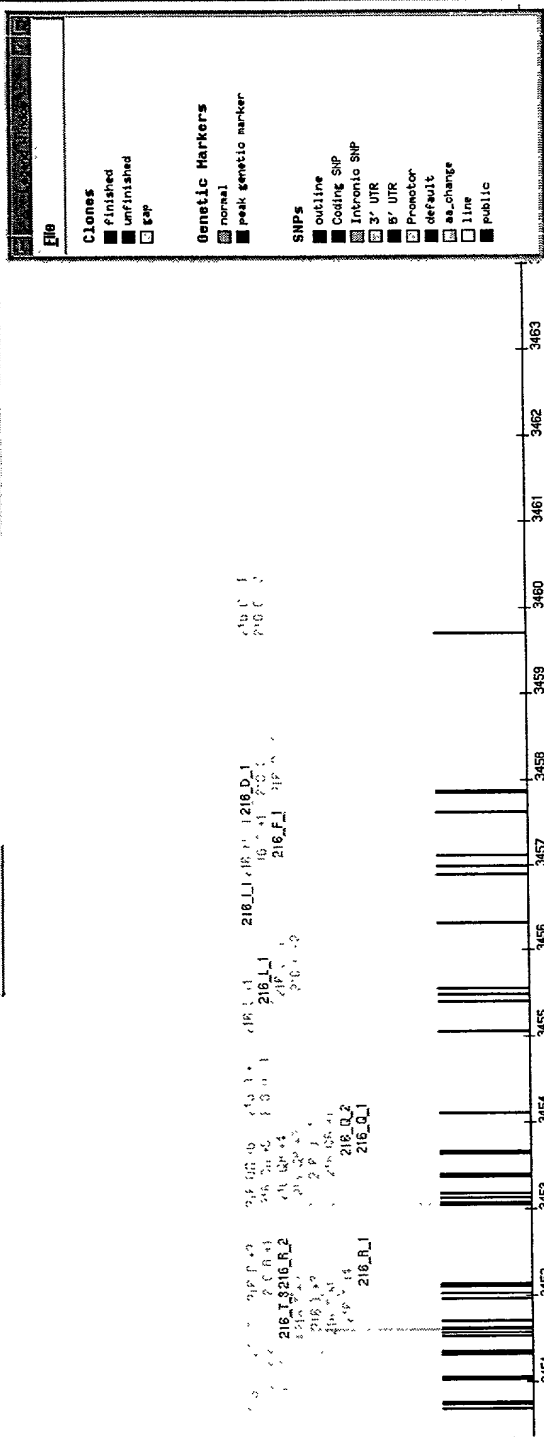


FIG. 9



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Gene216

216 promoter 216 mouse



FIG. 11

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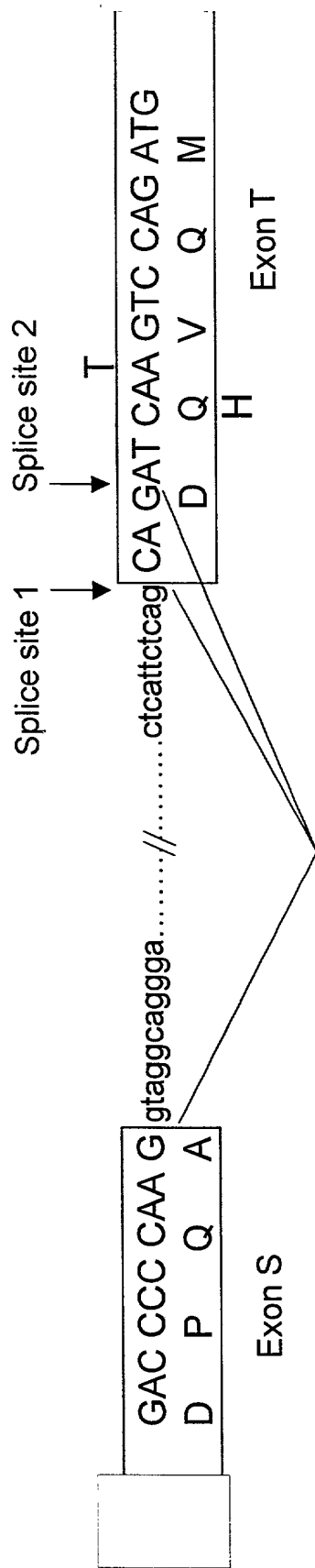


FIG. 12

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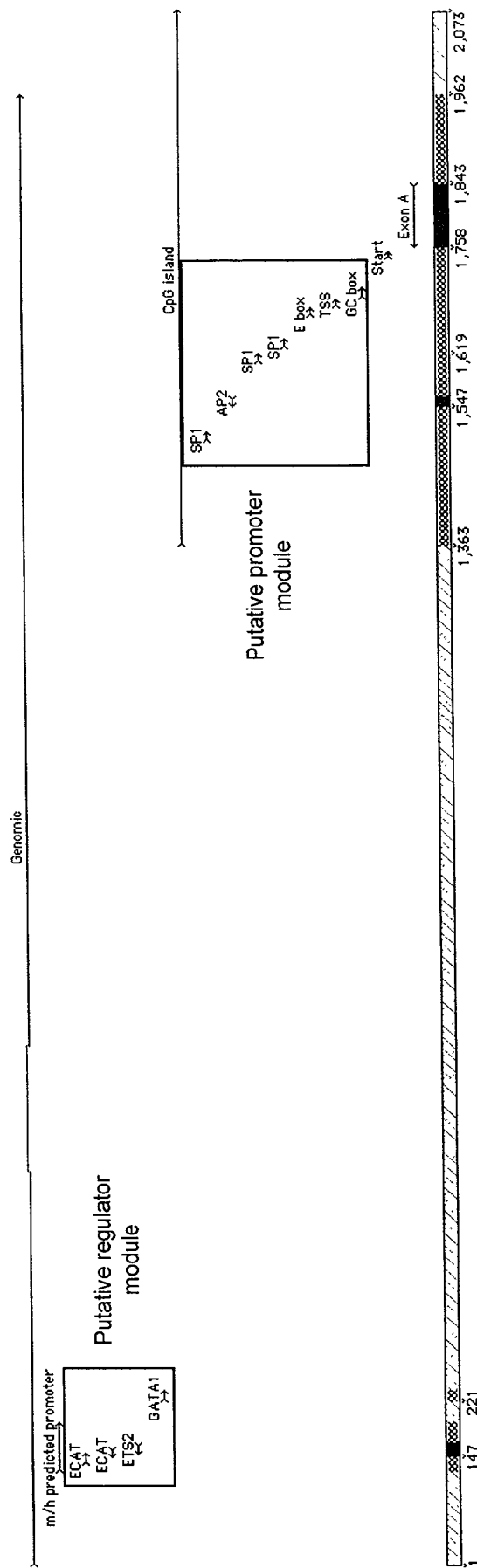


FIG. 13

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Branch of the ADAM family that Gene 216
is closely related to

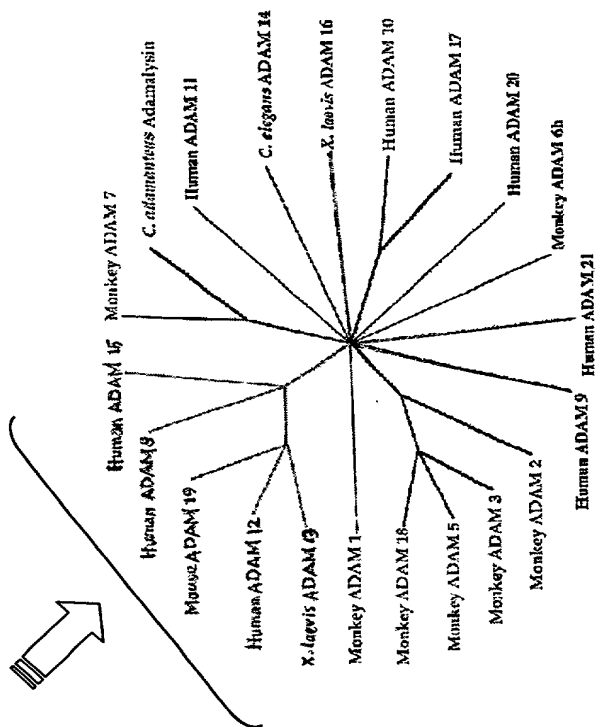


FIG. 14

Kb
 Brain
 Heart
 Sk. muscle
 Colon
 Thymus
 Spleen
 Kidney
 Liver
 Sm. Intestine
 Placenta
 Lung
 Leukocytes
 Spleen
 Lymph
 Thymus
 Leukocyte
 Bone marrow
 Liver
 ,
 Kb
 Bronchial smooth muscle

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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	1	2	3	4	5	6	7	8
A	Whole brain	Amygdala	Caudate nucleus	Cerebellum	Cerebral cortex	Frontal lobe	Hippocampus	Medulla oblongata
B	Occipital lobe	Putamen	Substantia nigra	Temporal lobe	Thalamus	Nucleus accumbens	Spinal cord	
C	Heart	Aorta	Skeletal muscle	Colon	Bladder	Uterus	Prostate	Stomach
D	Testis	Ovary	Pancreas	Pituitary gland	Adrenal gland	Thyroid gland	Salivary gland	Mammary gland
E	Kidney	Liver	Small intestine	Spleen	Thymus	Peripheral leukocyte	Lymph node	Bone marrow
F	Appendix	Lung	Trachea	Placenta				
G	Fetal brain	Fetal heart	Fetal kidney	Fetal liver	Fetal spleen	Fetal thymus	Fetal lung	
H	Yeast total RNA 100ng	Yeast tRNA 100ng	E.coli rRNA 100ng	E.coli DNA 100ng	Poly r(A) 100ng	Human Cot1 DNA 100ng	Human DNA 100ng	Human DNA 500ng

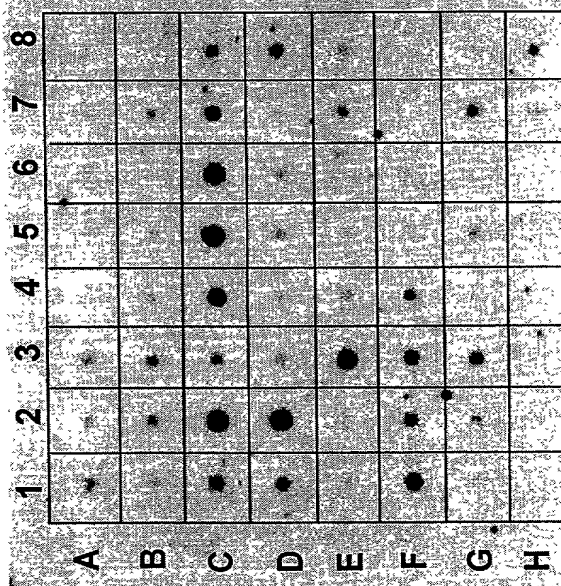


FIG. 16

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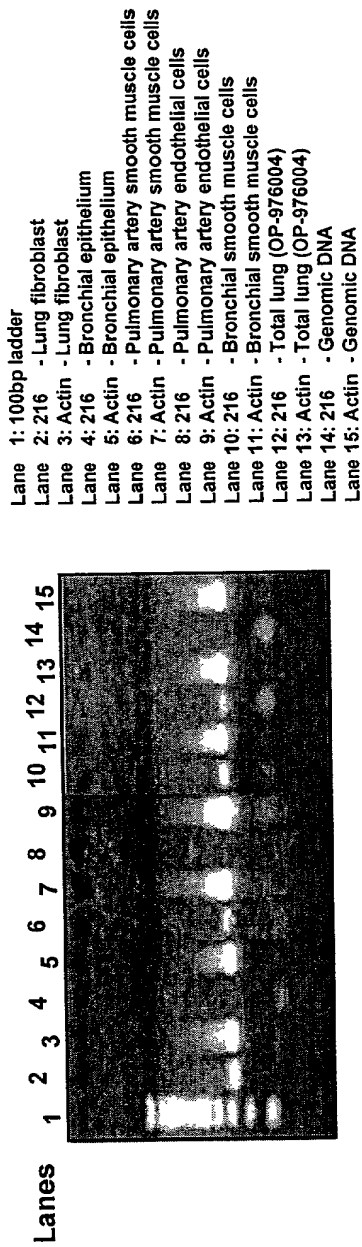


FIG. 17

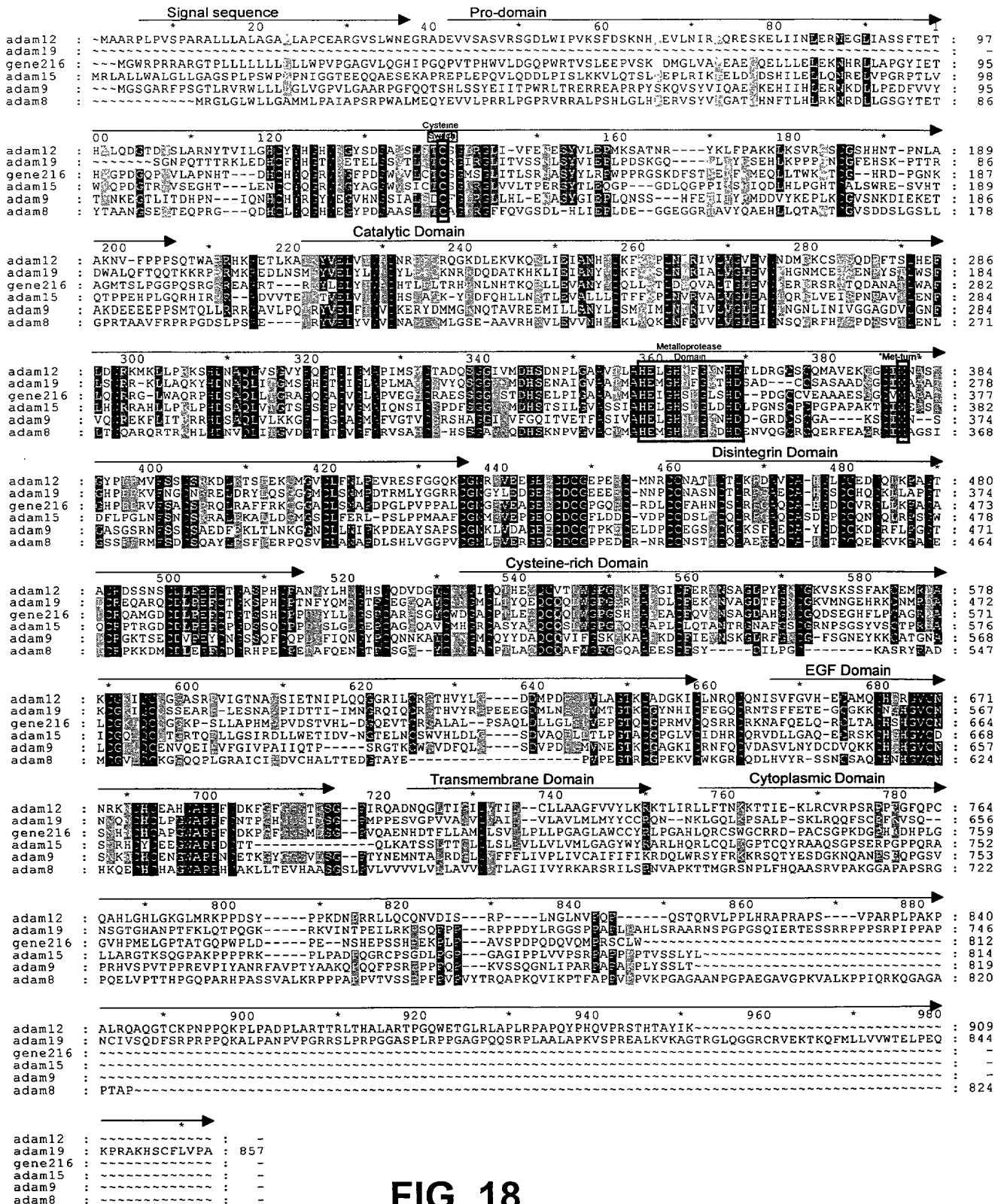


FIG. 18

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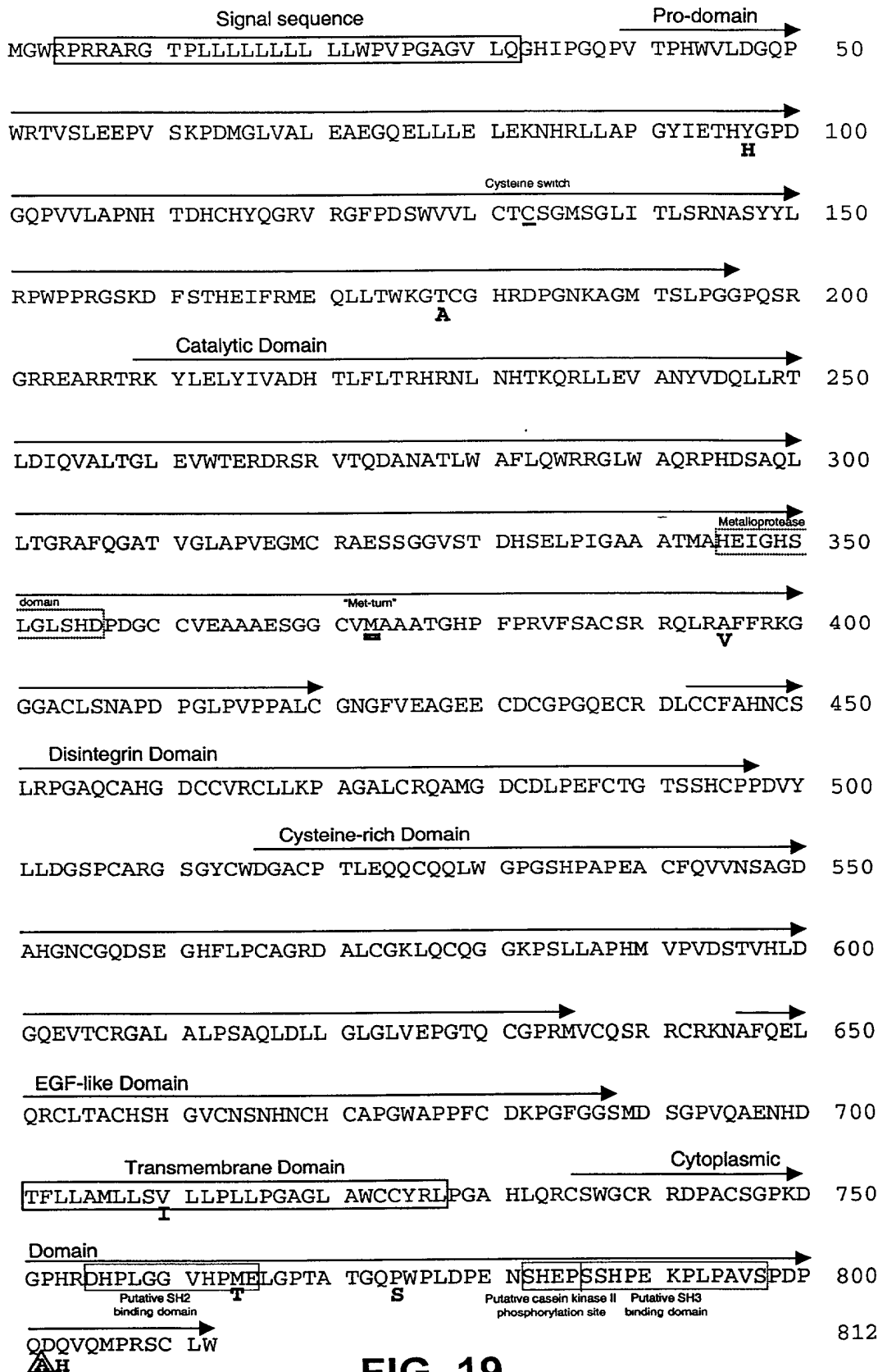


FIG. 19

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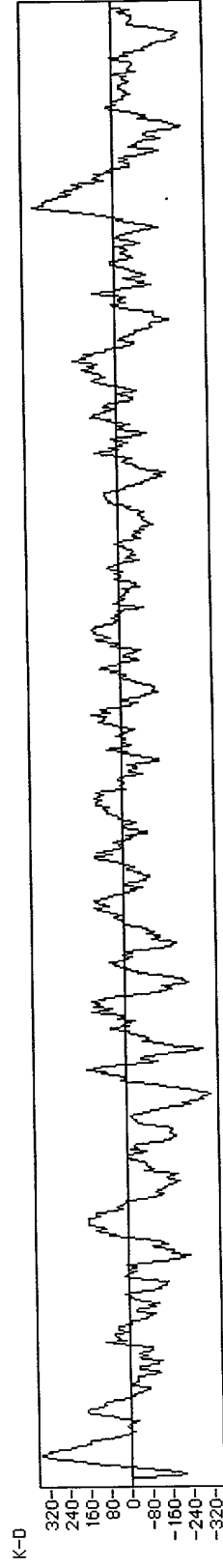
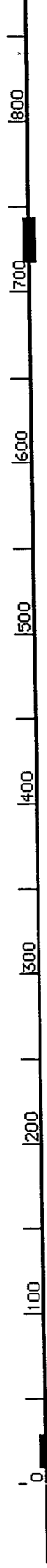


FIG. 20

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FIG. 21

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FIG. 21

FIG. 21

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FIG. 21

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FIG. 21

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FIG. 21

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tgtcttggaaaaaaaaaaagaggaagaaagaaaaagattttattttattttatacat
atgagtacaccatcagacacacaagaaggggcaccagaccccattacagatggttgta
gccaccatgtgggttgctgggaattgaactcaggacctctggaagaacagttgggtgctctt
aaccctgagccatctctccagcccaaatagatgatttcttaattcttaaggatgatcct
ataagaattcctaaacttacattagtaattattaagctcttttacaataggacttctatt
aagtcttctctaatatgaaaacttcaataagaactctgccagtcttcaagtgtcatgagt
tagttgcttctgagatagcaagtaggcatcaacaacttagagcacattctaggaggttg
aaaaccattaaccagtgggtcttaaaaagggaactaacaataggctatagggtgcaaggaca
gaagataaaatattgactaggtttatcaatacaaaaatttaccacaaaagttatgttttt
gacttttcataaaaaactctttatgaacctgtagaactgggtgaaagatgacgaatgcttag
ccagataattactcctaatagatatgcatgtgaatattctgtgctgtaaacttatttatg
tttgaacttccagtgaacttttgtttaaaaaaggggggggtgaaaaagccatgtgatc
tattctcctagaaagggtacagaagactaagaaagattacattggagatgtaaccttgga
gagaaagctttgggagcaagagcatagagagcaaggccattgtggcatcagagcaggagg

FIG. 21

agagagcaagattagaaggagatgcagagtggaataacttagaaactataaggcaacata
 aaaaattaagagagccatatgcagaatgcagagggaaagagaaaaaaaaaaaaaaaaaga
 agctgcagggagagcagaaggagcaggcaggcttctcctgaccatggggtagaacagggc
 ttttcttaataccaaggcaggcttagtcttaaggataataaagcttttctttcttacaga
 cttgggttttaattcatttagcaataaaaagtgtaaaagtgttttctttccctatgcaataa
 agattggagcttatttttcagccagaatgagtgagttctctctgcaacgggtgcttgggtct
 tttgcttcatatacacacataagtgtgtgtgtgctgcgcgcagctgctgtgtgtgtgtgtgtgt
 gtgtgtgtgtgtgtaagtgtgcaattatcagatggcatggaagctgggctcaattgggttc
 aaatggggacttgtgagggatatatgcatgaatctgtatatgaattcatgtgagcttatat
 atatttgcttgtgtaaaagtttttccttctgtgagtgactctcttctcctgggttcaat
 agaggtttattgcttcaaacttccccctagcctgacagtcgagaggcatctggacaagag
 agaaaaggetctagccattaatccttttcttagatccattttcttagagaactttcttag
 gaaactgttttagagagaacatagaaacaggctgaaatcacttgtcaaactgtccctttt
 ctctctaaggacttctactagcagactgggagtttagagctgcacagtccttgaggagata
 gaacaaaggctgctttactgaatccccctgctgttttaagatgaggttctaaaggagattg
 cagtttctgacccccaaaaggaaactcaggcaggctcagctacagtatcaaagtgacttaaa
 cttaaagataggatattgttttattattaaacagctaccctaaatatctcataagatcaag
 cttacccccggtgacacttccccctctgttgctcgaagaggaaccaagcagaaagaaccgc
 cagggctggctcctggcacaatgggttaaagatgttgtagcatggggaaatgaagagat
 ggctcagctattaagagaatatcttactcttcagaggaccagtggtcaattcccagcaa
 acatatcaggtgccacaccatcactttagctccagctgcagatctgctacatctggcct
 ccataggcaccacacacaggtggcaccacaaataaaaaataagataaatctaaaaca
 gcaaagttaaagcatgagctgaaactagtaaagtgttgtgtggcatagaccaagacctg
 ggtttggtccctacctgttagaaatagtctcagtatcacacaaaggaacacccaagcgaa
 gcaaaaagctcccagcaagacaaaactacagtcttcattgagagtgtgcacgctgaagacc
 gagcacactgggtgcaaaaatgtacttggattctgttttgcttgttttgttccagacaggg
 ttctctgcataacagccttggctgtccctgaaattcactgtgttagaccaggtggcctca
 aacctcagagatccgttcacccacgcttatctaggcttcagctctaccctgtgagatgg
 cctgaaagtgttagaaccgcgcgggatctatttctgacagactggctggcatcttttcc
 ttctctcagcatgagattcctggggcggttcccatttcagcatcaagcatggtagcagagt
 tggaacctgagggctgagggctcagactcagaccataaactggaagcagagagaactgga
 gattgtgggaggctttgaaacctcagctcctgccccagcaaataccttccagcaaggcca
 cacctcttaaacctccccaaacaggggtaccaactggggacctaatattcaaagtccac
 aaatatgggagacatgacatccaaaccgcccaggacaggtgtatacctccatgcttgggtt
 ccgtagtaagaaacactaaacattagcctttcctaataaaactgatataaagccctgct
 attctcgatgtttttctctgttctgtctcctccttctccacctgcttctctgttctctga
 cctcttctgtgtcacagatagccctgccatgtccatctgccagccatgttctgtctactt
 gcctctctctctgtctgtgactcttctagatgcctctggctgttctttctcatatctaca

FIG. 21

>mouse Gene 216 cDNA
AAAGGCACTCCCAGCCTATGGGCTCGAGGTGCGGGAGACCCGGGGGGTCTCCG
GTGCTGCTATGCTGCCGCTGTTGCTGCCCTCGTGTCCGCTGCGGAGCGCTCG
GATGTTTCCAGGAAATGCCCATGGAGAGCTAGTCACTCCCCACTGGATCCTGG
AGGGCAGACTCTGGCTCAAGGTCACCCTGGAGGAGCCGATCTTGAAGCCTGAC
TCGGTGCTGGTGGCTTTAGAGGCTGAAGGCCAGGATCTCCTGCTTGAAGTGA
GAAGAAGCACAAAGCTTCTGGCCCCAGGATACACAGAAACCCACTACAGGCCAG
ATGGGCATCCGGTAGTGCTGTCCCCAACCCACACGGATCATTGCCAATATCAC
GGGCGTGAGGGGCTTCCGGGAATCCTGGGTGGTCTCAGCACCTGCTCTG
GGATGAGTGGCCCTTATTGTGCTCAGCAGCAAAGTCAGCTATTATCTGCAACCTC
GGACTCCTGGGGATACCAAGACTTCCCAACCCACGAGATCTTCCGGATGGAG
CAGTTGTTACCTGGAGAGGGGTCCAGAGAGACAAGAACTCCCAATACAAAGC
AGGAATGGCCAGTCTTCTCATGTCCCCAGAGCCGGGTGAGGCGAGAGGCG
CGCAGGAGTCCCAGGTACCTGGAAGTGTACATAGTGGCTGACCACACCCCTGAA
CTTGAACACACGAGACAGCGCCTCCTGGAGGTTGCCAATTGCGTGGACCAGA
TTCTCAGGACTCTGATATACAGTTGGTGTGACCGGGCTGGAAGTGTGGACC
GAGCAGGATCTCAGTCGCATCACTCAGGACGCAAACGAAACGCTCTGGGCTTT
CCTACAGTGGCGCCGCGGGGTGTGGGCCAGGAGACCACGACTCCACACAA
CTGCTCACGGGCCGACCTTCCAGGGTACCACGGTGGGCTGGCACCTGTGG
AGGGCATATGCCGCGCGGAGAGCTCCGGAGGTGTGAGCACAGACCACTCGGA
ACTCCCCATCGGCACAGCAGCCACCATGGCCCACGAGATAGGCCACAGCCTGG
GCCTCCACCATGATCCCGAGGGCTGCTGCGTGCAGGCCGATGCAGAGCAAGG
AGGCTGCGTCATGGAGGCGACCCACAGGGCACCCCTTTCCCGCGCTCTTCAGCG
CCTGCAGCCGCGCCAGCTGCGCACCTTCTTCCGCAAAGGGGGCGGTCTTTGC
CTCTCCAACACCTCGGCGCCGGGGCTCCTGGTGCTGCCAGCCGCTGCGGAAA
CGGCTTCTTGAAGCAGGAGAAGAGTGCAGTGCAGTCTGGCCAGAAGTGC
CCGGACCCCTGCTGCTTTGCCCAATGCTCCCTGCGTGCGGGGGCTCAATG
TGCCACCGGTGATTGCTGTGCGAAGTGCCTGTTAAAGTCCGCGGGCACGCCTT
GTCGTCCTGCTGCGACTGACTGCGATCTCCCCGAGTTCTGCACCGGCACCTCC
CCGTATTGCCCCGCGAGATGTTTACCTACTGGATGGCTCACCTGCGCTGAGGG
TCGCGGCTATTGCCTAGACGGCTGGTGTCCCACGCTGGAGCAGCAGTGCCAGC
AGCTATGGGGGCTGGGTCCAAGCCGGCCCCAGAGCCATGTTTCCAGCAGAT
GAACTCCATGGGGAATTCGCAAGGGAACCTGTGGCCAGGACCACAAGGGTAGC
TTCCTGCCTTGTGCTCAGAGGGACGCTCTGTGTGGGAAACTGCTGTGCCAGGG
AGGGGAGCCGAACCCACTAGTGCCGCACATAGTACTATGGACTCCACAATTC
TCCTAGAGGGCCGCGAAGTGGTTTGCCGAGGGGCTTTGTGCTCCAGATAGT
CACCTGGACAGCTTGAAGTGGGTCTGGTAGAGCCAGGCACCGGCTGTGGACC
TAGAATGGTGTGCCAGGACAGGCACTGTGAGAATGCTACCTCCAGGAGCTGG
AACGTTGCTTGACTGCCTGCCATAACGGTGGGGTTTGCAATAGCAATCGTAAC
GTCAGTGTGCTGCTGGCTGGGCTCCACCCTTCTGTGACAAGCCTGGCTTGGGT
GGTAGCGTGGATAGTGGCCCTGCACAGTCTGCAACCCGAGATGCCTTCCCCTT
GGCCATGCTCCTCAGCTTCTGCTGCCTCTGCTCCCTGGGGCTGGCCTAGCCT
GGTGCTACTACAGCTCCCAACATTCTGTCTATCGAAGGGGACTGTGCTGCAGG
AGGGACCCCTATGGAATAGAGACATAACCCCTGGGCAGTGTGCATCCGGTGGA
GTTTGGCTCCATCATCACTGGAGAGCCCTCGCCCCCTCCCCATGGACCTCTTG
CCAACAGCGTTCGACCCCTCCATCTCTTGAAGTGTCTCAGACCCCTGCGAACTC
TGAGCTTACCTAAGAACTACCCCTCTGAAGCAGCCTGGTCTACAGATTGAGTTCC
AGACCTGCCCTATCCCTATGGTATGGAAGCACCCCTGAGGACCTCCTGTTGCCA
GTCACCTACCTCTGTCTCAGTTTGTGTCCCCTCCTCAGATTTACAGGCTTGCAT
CAATAAAGAAATGAGACATGGGCCCTCAGAGAASCTGTTGTCATAGAGACCATG
ATGCTGGAACCCCTAGGGGAGGGAAGGGAGACACTGTGGTCTTCTTGGGTC
CTTATAGAGGGAGGACAAATGTGCCCTGCCATGTGACTTGCAGTCCCTCAGTTTC
TCAGACGCACTCTTATAATTCTATGGGCTGTATGTGAGCTCTTACTCAGCATA
GGAACCCAGAGCCCGATCATGTTGTATCCSCCTGCCCTGAGAGCTGTGCTAT
TCTGAAATGTTAGAATGTATCTAATAACAATAAATCCACAAGTTATATCAGHAAA
AAAAAAA

FIG. 22

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>mouse Gene 216 protein

MGSRGPRGGSPVLLLLPLLLPSCPLRSARMFPGNAHGELVTPHWILEGRLWLKVTLEEPILKPDSVLVALEAEGQDLLL
ELEKKHKLLAPGYTETHYRPDGHVPVLSPNHTDHCQYHGRVRGFRSWVVLSTCSGMSGLIVLSSKVSYYLQPRTPGDTK
DFPTHEIFRMEQLFTWRGVQRDKNSQYKAGMASLPHVPQSRVRREARRSPRYLELYIVADHTLNLNHTRQRLLEVANCVD
QILRTLDIQLVLTGLEVWTEQDLSRITQDANETLWAFLOWRRGVWARRPHDSTQLLTGRTFQGTTVGLAPVEGICRAESS
GGVSTDHSELPIGTAATMAHEIGHSLGLHHDPEGCCVQADAEQGGCVMEAATGHFFPRVFSACSRRLRTFFRKGGGPCL
SNTSAPGLLVLPSCGNGFLEAGEECDGSGQKCPDPCFAHNCSLRAGAQAAGDCCAKCLLKSAGTPCRPAATDCDLP
EFCTGTSPYCPADVLLDGSPCAEGRGYCLDGWCPTLEQQCQQLWGPGSKPAPEPCFQQMNSMGNSQGNCGQDHKGSFLP
CAQRDALCGKLLCQGGEPNPLVPHIVTMDSTILLEGREVVCRGAFVLPDSHLDQLDLGLVEPGTGCGPRMVCQDRHCQNA
TSQELERCLTACHNGGVCNSNRNCHCAAGWAPPFCDKPGLGGSVDSGPAQSANRDAFPLAMLLSFLLPLLPAGLAWCY
QLPTFCHRRGLCCRRDPLWNRDIPLGSVHPVEFGSIITGEPSPPPPWTSCQQRSHPPSLDLLSDPANSELT

FIG. 22

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mGene216 582 VPHIVTMDSTILLEGREVVCRAFLPDSHLDQLDLGLVEPGTGCGPRMV 631
      |||. |. |||: |:|. | ||| | |. | | | | | | | | | | | |
hGene216 600 APHMVPVDSTVHLDGQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMV 649

mGene216 632 CQDRHCQNATSQELERCLTACHNGGVCNSNRNCHCAAGWAPPFCDKPGLG 681
      || | |. |||: ||| | |. | | | | | | | | | | | | | |
hGene216 650 CQSRRRCRKNAFQELQRCLTACHSHGVCNSNHNCHCAPGWAPPFCDKPGFG 699

mGene216 682 GSVDSGPAQSANRDAFPLAMLLSFLLPLLPGAGLAWCYQLP.TFCHRRG 730
      |||. ||| |. | | | | | | | | | | | | | | | |. | | |
hGene216 700 GSMDSGPVQAENHDTFLLAMLLSVLLPLLPGAGLAWCCYRLPGAHLQRCS 749

mGene216 731 LCCRRDPLW.....NRDIPLGSVHPVEFGSIITGEPSPPPPWTSCQQR 773
      |||| | | | | | | | | | | | | | | | | | | | | :
hGene216 750 WGCRRDPACSGPKDGPGRDHPLGGVHPMELGPTATGQPWPLDPENSHEPS 799

mGene216 774 SHP..PSLDLLSDPANSELT..... 791
      ||| | |. | | :.
hGene216 800 SHPEKPLPAVSPDPQADQVQMPRSCLW 826

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FIG. 23

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      10              30              50
CGGGCACGGGTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG
-----+-----+-----+-----+-----+-----+-----+-----+
      70              90              110
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGC
-----+-----+-----+-----+-----+-----+-----+
                      MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

      130             150             170
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGAC
-----+-----+-----+-----+-----+-----+-----+
euLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

      190             210             230
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTCTGGATGGACAACCCTGGCGCACCCG
-----+-----+-----+-----+-----+-----+-----+
isIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThrV

      250             270             290
TCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAG
-----+-----+-----+-----+-----+-----+-----+
alSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluG

      310             330             350
GCCAGGAGCTCCTTGCTTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAG
-----+-----+-----+-----+-----+-----+-----+
lyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleG

      370             390             410
AAACCCACTACGGCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGTGAGAT
-----+-----+-----+-----+-----+-----+-----+
luThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrValArgC

      430             450             470
GCTTCCATGGGCTCTGGGATGCACCGCCAGAGGATCATTGCCACTACCAAGGGCGAGTAA
-----+-----+-----+-----+-----+-----+-----+
ysPheHisGlyLeuTrpAspAlaProProGluAspHisCysHisTyrGlnGlyArgValA

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FIG. 24

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```

      490              510              530
      .               .               .
GGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCA
-----+-----+-----+-----+-----+-----+-----+
rgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIleT

      550              570              590
      .               .               .
CCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACT
-----+-----+-----+-----+-----+-----+-----+
hrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspP

      610              630              650
      .               .               .
TCTCAACCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCC
-----+-----+-----+-----+-----+-----+-----+
heSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyH

      670              690              710
      .               .               .
ACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGGG
-----+-----+-----+-----+-----+-----+-----+
isArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArgG

      730              750              770
      .               .               .
GCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACA
-----+-----+-----+-----+-----+-----+-----+
lyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHist

      790              810              830
      .               .               .
CCCTGTTCTTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCG
-----+-----+-----+-----+-----+-----+-----+
hrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValA

      850              870              890
      .               .               .
CCAACCTACGTGGACCAGCTTCTCAGGACTCTGGACATTGAGGTGGCGCTGACCGGCCTGG
-----+-----+-----+-----+-----+-----+-----+
laAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeuG

      910              930              950
      .               .               .
AGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGG
-----+-----+-----+-----+-----+-----+-----+
luValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrpA

      970              990             1010

```

FIG. 24

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```

CCTTCCTGCAGTGGCGCCGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGC
-----+-----+-----+-----+-----+-----+
laPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeuL

      1030              1050              1070
TCACGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCC
-----+-----+-----+-----+-----+-----+
euThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCysA

      1090              1110              1130
GCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCCGCAG
-----+-----+-----+-----+-----+-----+
rgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAlaA

      1150              1170              1190
CCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCT
-----+-----+-----+-----+-----+-----+
laThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCysC

      1210              1230              1250
GCGTGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGT
-----+-----+-----+-----+-----+-----+
ysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisProp

      1270              1290              1310
TTCCGCGCGTGTTCAGCGCCTGCAGCCGCCGCGAGCTGCGCGCTTCTTCCGCAAGGGGG
-----+-----+-----+-----+-----+-----+
heProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGlyG

      1330              1350              1370
GCGGCGCTTGCCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGCG
-----+-----+-----+-----+-----+-----+
lyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCysG

      1390              1410              1430
GGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCGCG
-----+-----+-----+-----+-----+-----+
lyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArgA

      1450              1470              1490

```

FIG. 24

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ACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCGGGGGCCAGTGCGCCACGGGG
 -----+-----+-----+-----+-----+-----+
 spLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGlyA

1510 1530 1550
 ACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTG
 -----+-----+-----+-----+-----+-----+
 spCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGlyA

1570 1590 1610
 ACTGTGACCTCCCTGAGTTTTGCACGGGCACCTCCTCCCAGTGTCCCCAGACGTTTACC
 -----+-----+-----+-----+-----+-----+
 spCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyrL

1630 1650 1670
 TACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCCA
 -----+-----+-----+-----+-----+-----+
 euLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysProT

1690 1710 1730
 CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACCCAGCTCCCGAGGCCT
 -----+-----+-----+-----+-----+-----+
 hrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAlaC

1750 1770 1790
 GTTTCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGG
 -----+-----+-----+-----+-----+-----+
 ysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGluG

1810 1830 1850
 GCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTG
 -----+-----+-----+-----+-----+-----+
 lyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGlyG

1870 1890 1910
 GAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTACCTAGATG
 -----+-----+-----+-----+-----+-----+
 lyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAspG

1930 1950 1970
 GCCAGGAAGTGACTTGTGCGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTG

FIG. 24

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```

-----+-----+-----+-----+-----+-----+
lyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuLeuG

      1990              2010              2030
GCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGAGCAGGC
-----+-----+-----+-----+-----+
lyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnSerArgA

      2050              2070              2090
GCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACG
-----+-----+-----+-----+-----+
rgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisG

      2110              2130              2150
GGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTG
-----+-----+-----+-----+-----+
lyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProPheCysA

      2170              2190              2210
ACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACA
-----+-----+-----+-----+-----+
spLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnHisAspT

      2230              2250              2270
CCTTCCTGCTGGCCATGCTCCTCAGCGTCTCTGCTGCCTCTGCTCCCAGGGGCCGGCCTGG
-----+-----+-----+-----+-----+
hrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuA

      2290              2310              2330
CCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAA
-----+-----+-----+-----+-----+
laTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgA

      2350              2370              2390
GGGACCCTGCGTGTCAGTGGCCCCAAAGATGGCCCACACAGGGACCACCCCCTGGGCGGCG
-----+-----+-----+-----+-----+
rgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGlyV

      2410              2430              2450
TTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCTGGACCCTGAGA
-----+-----+-----+-----+-----+

```

FIG. 24

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alHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspProGluA

2470 2490 2510
 ACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCC
 -----+-----+-----+-----+-----+
 snSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProAspProG

2530 2550 2570
 AAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGA
 -----+-----+-----+-----+-----+
 lnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

2590 2610 2630
 ACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAAGTGCAGGGGCAG
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

2650 2670 2690
 AGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAAGTTTCTTCCCCGAGT
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

2710 2730 2750
 GGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATAGAAAGTTCTGAGGGCTGG
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

2770 2790 2810
 AGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCA
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

2830 2850 2870
 CACAGCCCCTGACCTCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAGGGC
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

2890 2910 2930
 TCTGTCTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCACGGACCCAGCTCTGTGGA
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

2950 2970 2990
 GGGCATGACTGCTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTCCAC
 -----+-----+-----+-----+-----+
 -----+-----+-----+-----+-----+

FIG. 24

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```

      3010              3030              3050
ACTCCCCTGCAGCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCCTTCCT
-----+-----+-----+-----+-----+-----+-----+

      3070              3090              3110
GTTTCTTCCCACCCTGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCACCCCAATCCCAG
-----+-----+-----+-----+-----+-----+-----+

      3130              3150              3170
TGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATTTCTGTGTGTGT
-----+-----+-----+-----+-----+-----+-----+

      3190              3210              3230
CGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAGAAAGACA
-----+-----+-----+-----+-----+-----+-----+

      3250              3270              3290
TGTTGGCTATAGGCGTGGTGGCTCATGCCCTATAATCCCAGCACTTTGGGAAGCCGGGGTA
-----+-----+-----+-----+-----+-----+-----+

      3310              3330              3350
GGAGGATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCA
-----+-----+-----+-----+-----+-----+-----+

      3370              3390              3410
TCTACAGAAAAATTTTAAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGC
-----+-----+-----+-----+-----+-----+-----+

      3430              3450              3470
TCAGGAGGCTGAAGCAGGAGGATCAGTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGG
-----+-----+-----+-----+-----+-----+-----+

      3490              3510              3530
TGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAAATAAATTTT
-----+-----+-----+-----+-----+-----+-----+

      3550              3570              3590

```

FIG. 24

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AAAAAGACATAA
-----+-----+-----+-----+-----+-----+

3610

AAAAAAAAAAAAAAAAAAAAAAAAA
-----+-----+

FIG. 24

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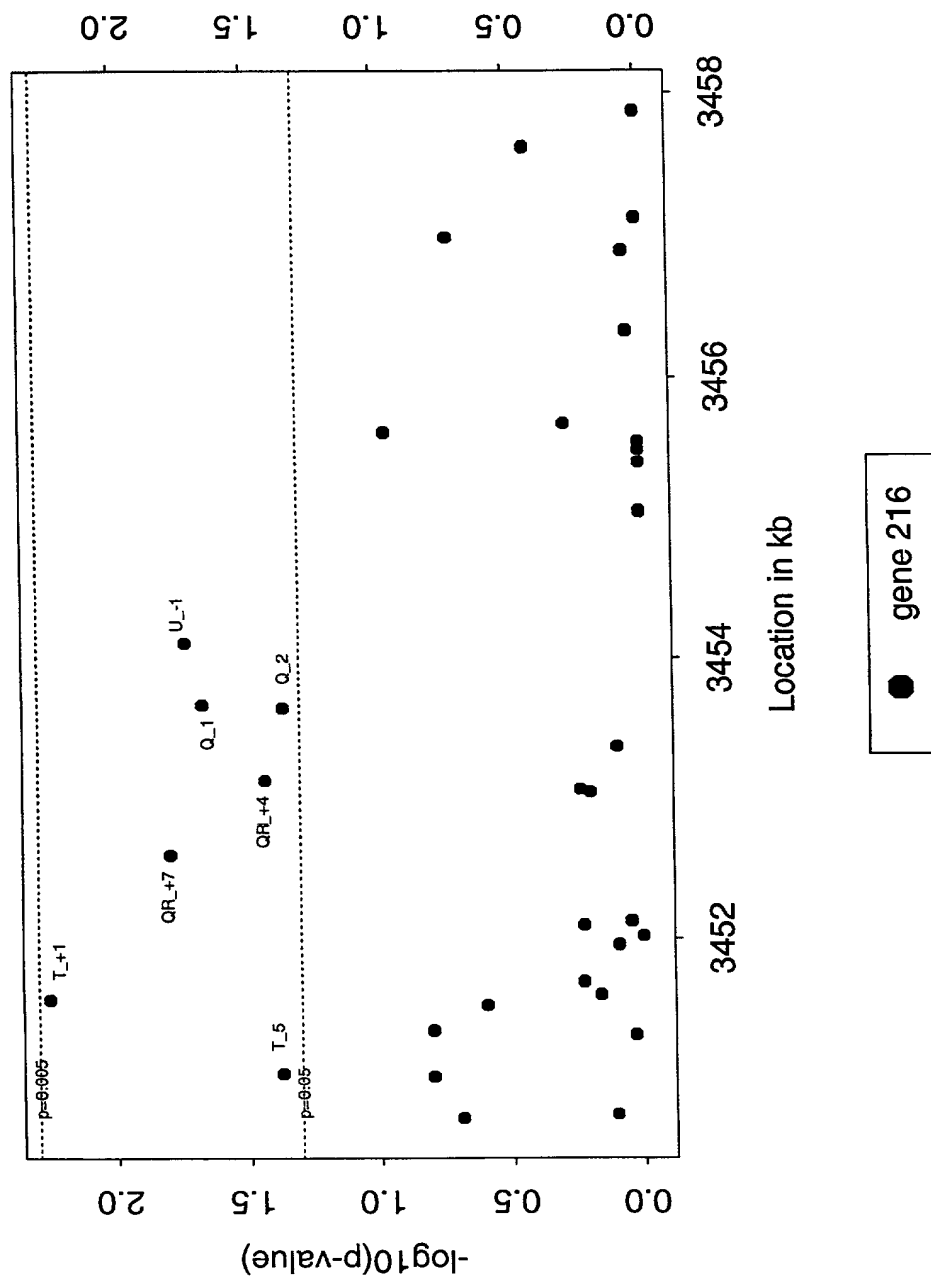


FIG. 25

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US

UK

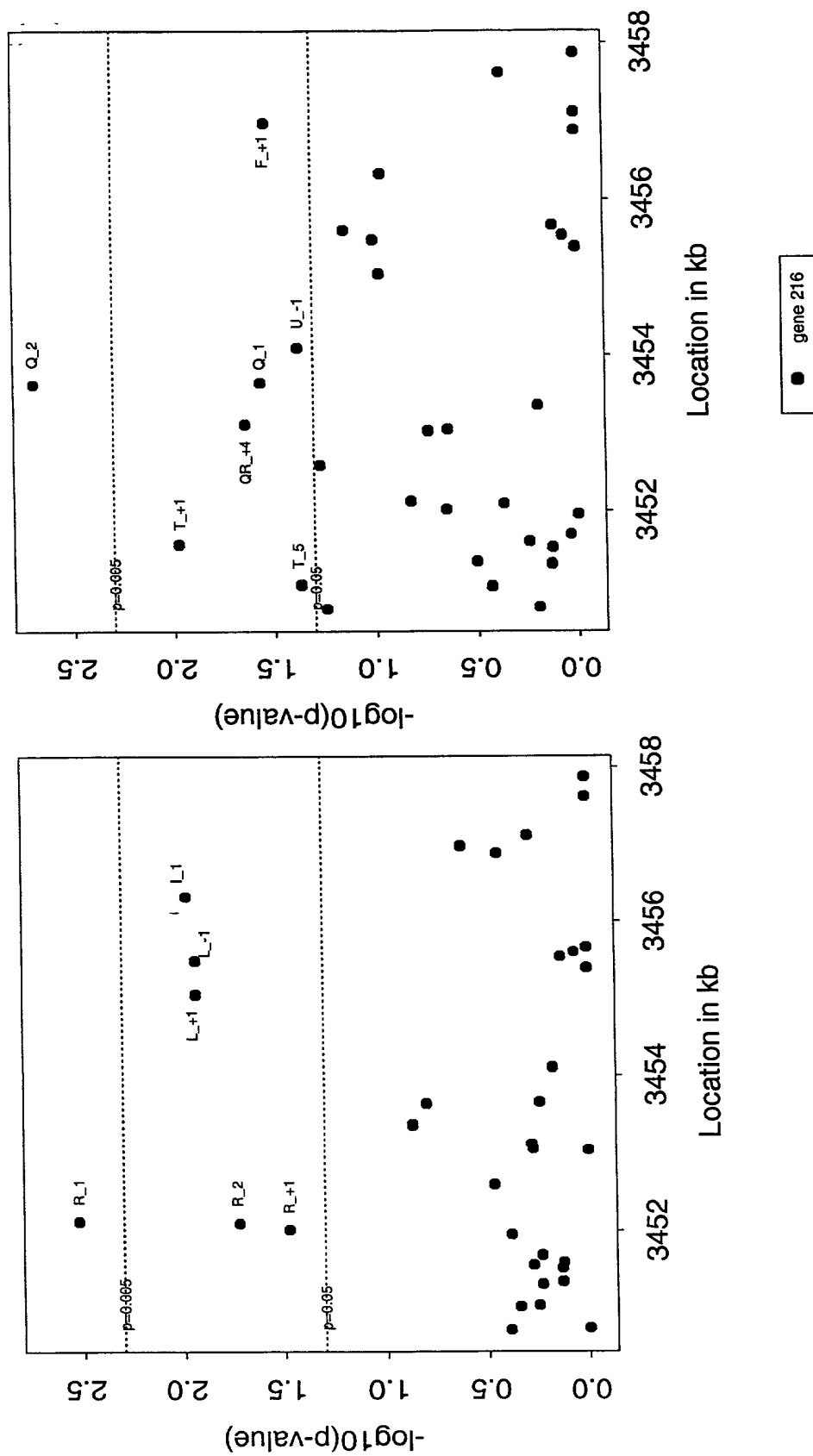


FIG. 26

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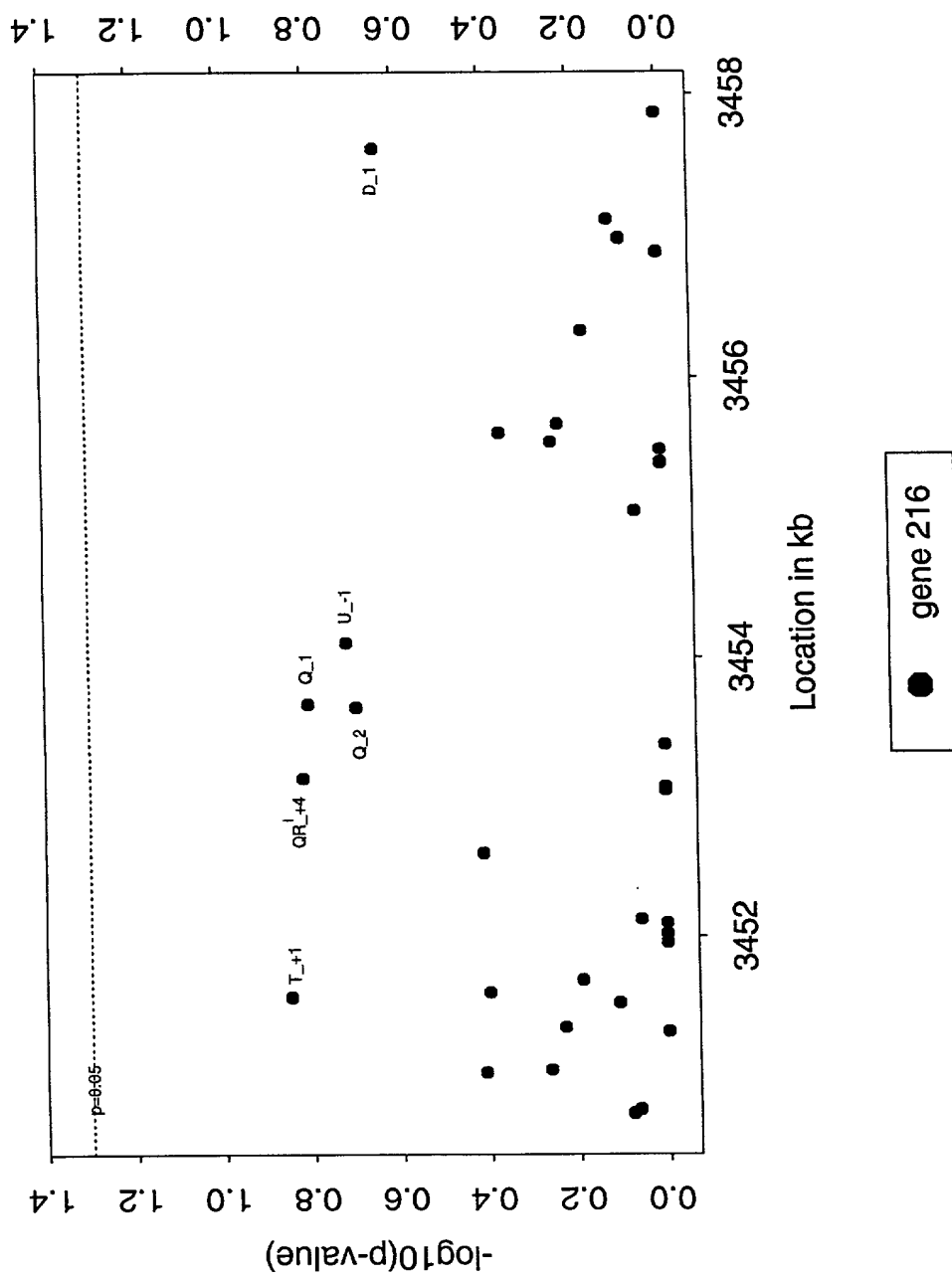


FIG. 27

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US

UK

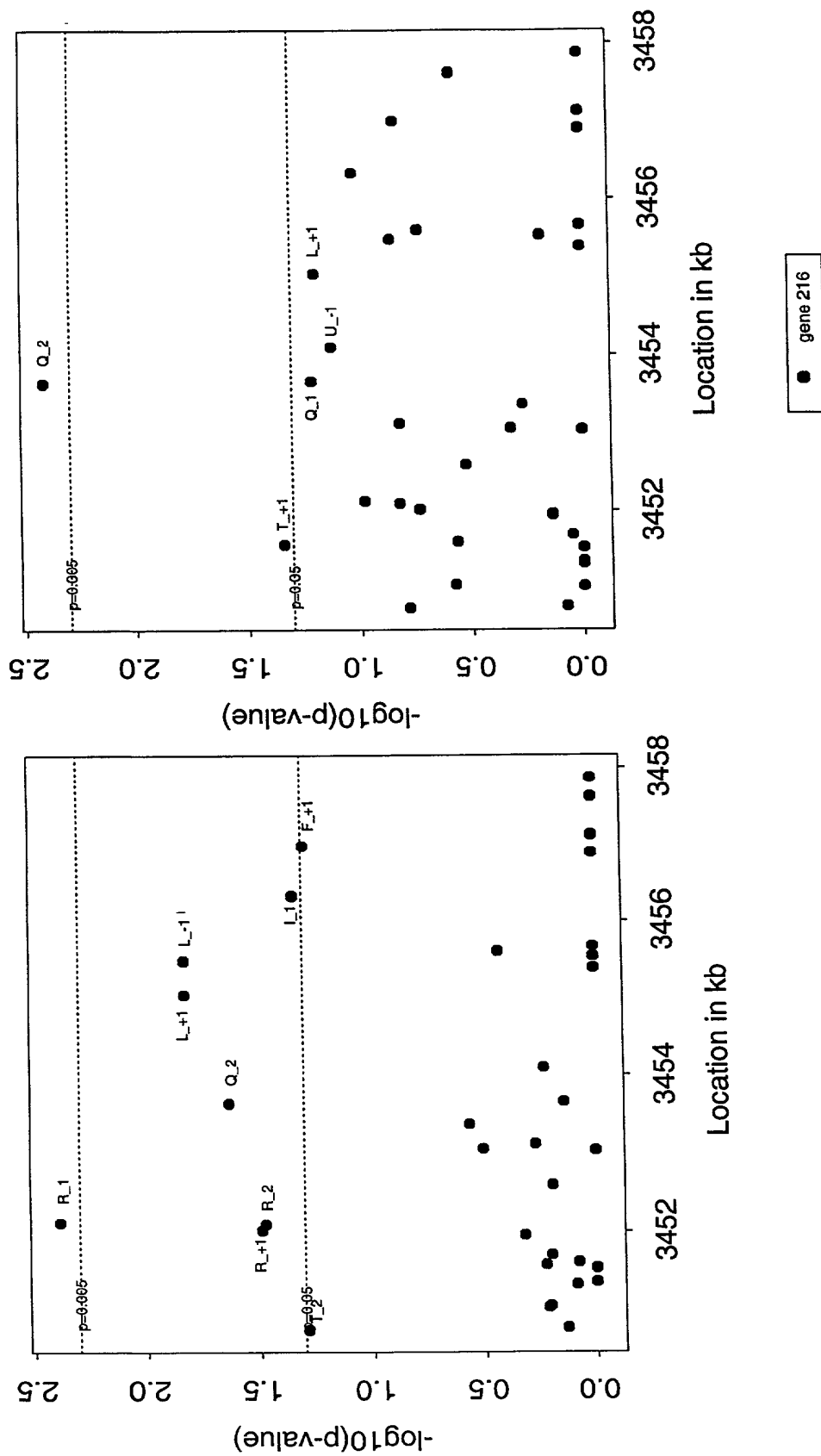


FIG. 28

Parameter	Value	Unit	Comment
α	0.0000	deg	Right ascension
δ	0.0000	deg	Declination
λ	0.0000	deg	Longitude
b	0.0000	deg	Barycentric latitude
ϕ	0.0000	deg	Phase angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η	0.0000	deg	Eta angle
ζ	0.0000	deg	Zeta angle
ξ	0.0000	deg	Xi angle
\omicron	0.0000	deg	Omega angle
κ	0.0000	deg	Kappa angle
ι	0.0000	deg	Iota angle
θ	0.0000	deg	Theta angle
ψ	0.0000	deg	Psi angle
χ	0.0000	deg	Chi angle
η			

FIG. 29

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GCTTCCAGTGGTCTGAGGCCTCTGAGACTTTTTGTACATTCAATTAAAGTGTAACATAC
-----+-----+-----+-----+-----+-----+-----+
610 630 650
AGAAAAGTTCACACATTATAAATGCAACTCAAGGACTTTTCCAAAAGCGAACACACCCAG
-----+-----+-----+-----+-----+-----+-----+
670 690 710
ATCAAGAAATAGACCATCCTACAGTCCCCCTTACACTCTGTACCAGTTGCAGCCCCAC
-----+-----+-----+-----+-----+-----+-----+
730 750 770
AAGGGTAACTACTGTCTTGACTTCGAACACCATAGATTGATTTGCCTGTTTTTAAACTT
-----+-----+-----+-----+-----+-----+-----+
790 810 830
TACATAAGTAGAATCACAGAGTGTGTACAATGACTTTGGAAAAGTGTGACAATATCTA
-----+-----+-----+-----+-----+-----+-----+
850 870 890
TTAAAGCTAAAATACCCTTGCCCTATGAACCTGAAATTCCACCCACCTTGCCAAGGGACA
-----+-----+-----+-----+-----+-----+-----+
910 930 950
AAAAGTTCCTCTAAATGCACCAGGCTGTGAGGATGAAGCGTTGGCTTTGGGGCCCCC
-----+-----+-----+-----+-----+-----+-----+
970 990 1010
ATTACACACATGACCTTTTCTGGGGCACCAAGCATCAGCCTGTCGTACCAGGTGCCA
-----+-----+-----+-----+-----+-----+-----+
1030 1050 1070
CCCTGGCGATCTCTGAAGGCTGGAGTCGGAGTGCCTCCCTCAGACATCCTGTTCTGCGTC
-----+-----+-----+-----+-----+-----+-----+
1090 1110 1130
ACTCCTTGGGAGAAGTCGTGTTTACAGATGGTGGGTGTCACCCATGCCAAGCACTTCTAA
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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1150 1170 1190
GGGTTAATGCTCACTGGTTTGCCTGGTTCCCAGGACATTTCTGATGCCCCTCTGGAGGG
-----+-----+-----+-----+-----+-----+-----+
1210 1230 1250
TGACGCCAACAAAGCCAGTGGAGAAGCCATCTTTCCCAGGTGCTGTCTAGGCGCCCCGGAG
-----+-----+-----+-----+-----+-----+-----+
1270 1290 1310
CTGCTCGGTGCATCCTAGGATCCCTCTTCCTCAGCTTTGGTTTGATGGCCTCATCTCCTC
-----+-----+-----+-----+-----+-----+-----+
1330 1350 1370
CCCTGCAACCTCAAAATGTAAATAAACCTTTCTCAGAGACTTCGGCAGAAAATTCCTCT
-----+-----+-----+-----+-----+-----+-----+
1390 1410 1430
GACCTGCACTTGGACACAGCTCATCTGGGTTTGGGAGGTGCTCAACTGTGTAAGGATGACT
-----+-----+-----+-----+-----+-----+-----+
1450 1470 1490
CTGATCCCCATGTGGCTTTTCGACTGTGTCCCCTCTACAGTCAGTTATTAGCACTGACTG
-----+-----+-----+-----+-----+-----+-----+
1510 1530 1550
TGCTAGGAAGTGAGCAACACACATATTTCCAGACCACATGGAGCTCAGGAGCTTGGGGAG
-----+-----+-----+-----+-----+-----+-----+
1570 1590 1610
AGAGACAGGGAAGTGGACGACTACAGGGCCTTCTGAAACGTGTTGCAGGGAGAAGTGTCA
-----+-----+-----+-----+-----+-----+-----+
1630 1650 1670
GTCAGGGGATGCTAACCTGGCTTTGGGTAAGGGACAGCCTCTGAATGACAGGACATTAAA
-----+-----+-----+-----+-----+-----+-----+
1690 1710 1730

FIG. 29

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GCCATGGCCTGCAGTTTAAAGTAGGAGTTGGCCAGTTCGAGGTAAGAATACCAGTAAGCAA
-----+-----+-----+-----+-----+-----+-----+

1750

1770

1790

GAACGCCAGAGTAGCTCCTCGAGCTGCCTTCTGTACCTGACATCCACACTGAAGCCAGCC
-----+-----+-----+-----+-----+-----+-----+

1810

1830

1850

CCTCTGTGTTTCAGCCTTGCTTTACTGAAGAGGTGTCGCTGAGGGGCTGCTCTGGGGTGCT
-----+-----+-----+-----+-----+-----+-----+

1870

1890

1910

GCTCTGCTTTTCTGTCCCAACTTGTCTGAGCTCGAGCCACCTCCATACTGGTGCTCCT
-----+-----+-----+-----+-----+-----+-----+

1930

1950

1970

GGTTCTCAGGCCTTTGAACTCAAACCTGAATCACACCACTGGCTTTCCTCGTTCTCCAGCT
-----+-----+-----+-----+-----+-----+-----+

1990

2010

2030

TGCAGATGGCAGATTTCGGAACTTTTTGGCCTCCATAATCACGTGAGCCAATTGCTATAA
-----+-----+-----+-----+-----+-----+-----+

2050

2070

2090

TAAATATCTCTCTCCCTCTTTCTTCTCTCTCTCTCTCTGTGCAAATATAGTTCCAATTA
-----+-----+-----+-----+-----+-----+-----+

2110

2130

2150

TAAGAGCCCCTAACTGGAAAATAACCCTATGGTGCACTGGTGAGTAGAGAACTGTGGTT
-----+-----+-----+-----+-----+-----+-----+

2170

2190

2210

CCCTCAAACCACCGAACACTATTCAGCAATACGAAGGAACAACTATTGATATGCAAAA
-----+-----+-----+-----+-----+-----+-----+

2230

2250

2270

AGTGTAATGAATCTCAAAAACATCGGAAAGAGGGAAGGAAGCCAGACACAGAAGAGTGC
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```

2290          2310          2330
ATGCCGCATGATTCCATTTATATGAAATTCTAGAACAGGCAAACTTATCTATAGACAGA
-----+-----+-----+-----+-----+-----+-----+

2350          2370          2390
GAACAACAGATCAGTGGCTGTCTGGGGTTGGGAGTGGGGAAGTTTGGCTGGAAGGGCACAA
-----+-----+-----+-----+-----+-----+-----+

2410          2430          2450
GGGCTCTTTCTGTGAGTGAGGGAATGTGTCTGCATTATAGTGATGCTTATGTAGTTATAT
-----+-----+-----+-----+-----+-----+-----+

2470          2490          2510
ACACTTATCGAAACTCATCTTACTGGCCACTTAAAATAAGTGCATTTTATTGTGTGTAA
-----+-----+-----+-----+-----+-----+-----+

2530          2550          2570
TTATACCTTAATGAAGTTGATTTGAAAATCCAAAGTAGTAATAATAAGTAATAATCTCGT
-----+-----+-----+-----+-----+-----+-----+

2590          2610          2630
AGCTGGACAGCTGTGGTGACTCACTCCTGTAATTCCAGCGATTTGAGAAGCTGAGGCAGG
-----+-----+-----+-----+-----+-----+-----+

2650          2670          2690
AGGATCACTTAAGATCAGGAGTTCTTTTTATTTTATTTTATTTTATTTTGGAGACGGAGTT
-----+-----+-----+-----+-----+-----+-----+

2710          2730          2750
CGCTCTTGTGCCCAGGCTGGAGTGCAATGGCATGATCTCGGCTCGCTGCAACCTCCACC
-----+-----+-----+-----+-----+-----+-----+

2770          2790          2810
TTCTGAGTTCAAGCGATTTTCTGCCTCAGCCTCCCAAGTAGCTGGAACCTACAGGCGCTC
-----+-----+-----+-----+-----+-----+-----+

2830          2850          2870
```

FIG. 29

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ACCACCATGCCCGGCTAATTTTGTATTTTAGTAGAGATGGGGTTTCACCATGTTGGCC
-----+-----+-----+-----+-----+-----+-----+
2890 2910 2930
AGACTGGTCTTGAACCTCTGACCTCCAGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTG
-----+-----+-----+-----+-----+-----+-----+
2950 2970 2990
GGATTACAGGCATGAGACACTGCGCCTGGCCAAGACCAGGAGTTTGAGACCAGCCTGGGA
-----+-----+-----+-----+-----+-----+-----+
3010 3030 3050
AACAAAGTGAGACCCCTGTCTACAGAAAAATTAAAAATTTAGCTGGGCCTGGTGCCGT
-----+-----+-----+-----+-----+-----+-----+
3070 3090 3110
GTGCCTGTAGTTCCAGCTACTCAGGAGGCTGAGGTGGGAGGATACCTTGAGCCCAGGATT
-----+-----+-----+-----+-----+-----+-----+
3130 3150 3170
TCAAGGCTGCAATGAGGCATGATCAGGCCACTGTCCTCTAGCGTGGGTGACAGAGTGAGA
-----+-----+-----+-----+-----+-----+-----+
3190 3210 3230
CCCTGTCTCTAAATAATAATCATAAGAACAACAAGGACCTCTAAACGCACTGATATCTA
-----+-----+-----+-----+-----+-----+-----+
3250 3270 3290
AGGTGTATTAAGCGACCAAAAAAAAAAAGAAAATCAAAGTGCAGAAAAACGTTAATAAGA
-----+-----+-----+-----+-----+-----+-----+
3310 3330 3350
GAAAAAATATGTCTGTATTGTCTTGAGTGTGAAAAATAATCTAAAGCCTATGAAAGA
-----+-----+-----+-----+-----+-----+-----+
3370 3390 3410
AACTAATCATATTGGTTTCCTGTTGGTGAGGAGGGCTAAGAGCACGGAGACTTTTCCCTA
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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3430 3450 3470
TGCTTTCTGTACTTTTTGATTTTGAGATATGTGAATGTAGGTTTCTCTCACTGCTCGAAC
-----+-----+-----+-----+-----+-----+-----+
3490 3510 3530
TTTCACTAACCAAATTACTACATTCCAAATTCTCAAAAACAAATAGATTTACTTAAAAGT
-----+-----+-----+-----+-----+-----+-----+
3550 3570 3590
AGGCTGGGTGCGGTGTCTCACGCCTGTAATTCCAGCGCTTTGGGAGGCCGAGGCGGGCAG
-----+-----+-----+-----+-----+-----+-----+
3610 3630 3650
ATCACCTGAGGTCTGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAACCCATCTCTAC
-----+-----+-----+-----+-----+-----+-----+
3670 3690 3710
TAAAAATACAAAATTAGCCAGGCGTGGTGGCGAATGCCTGTAATGCCAGCTACTCGGGAG
-----+-----+-----+-----+-----+-----+-----+
3730 3750 3770
GCTGAGGCAGAAGAATCACTTGAATCTGGGAGGCAGAGGTTGCAGTGAGCCCAGATCATG
-----+-----+-----+-----+-----+-----+-----+
3790 3810 3830
CCATTGCACTCCAGTCTGGGTAACAAGAGAGAACTCTGTCTCAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+
3850 3870 3890
AAAAGATTTGCTTAAAAGTTAACATCTCCGGCCGGGCGCGGTGGCTCATGCCTGTAATCC
-----+-----+-----+-----+-----+-----+-----+
3910 3930 3950
CAGCGCTTTGAGAGGCCGAGGCGGGTGGATCACGAGATCAGGAGATTGAGACCATCCTGG
-----+-----+-----+-----+-----+-----+-----+
3970 3990 4010

FIG. 29

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```
CCAAAATGGTGAAACCTCGTCTCTGCTAAAAATACAAAAGTTAGCTGGGGGTGGTAGCGC
-----+-----+-----+-----+-----+-----+-----+
4030          4050          4070
GCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGT
-----+-----+-----+-----+-----+-----+-----+
4090          4110          4130
CGGAGGTTGCAGTGAGCCAAGATCGCGCCGCTGCACTCCAGCCTGGCGACAGAGGGAGAC
-----+-----+-----+-----+-----+-----+-----+
4150          4170          4190
TCCATCTCAAAAAAAAAAAAAAAAAAAGTTAACATCTCATCCAAATTTGCACCGAGTA
-----+-----+-----+-----+-----+-----+-----+
4210          4230          4250
GGAAAACAAAAGTTTAAACATGAAACAGATGTTACTGAGGCCGAAAGGGTCTCCCAGGC
-----+-----+-----+-----+-----+-----+-----+
4270          4290          4310
CTGGGAGTCTGCAGCTTTTATGCAATTCTGCCCTCTGGCCACCGCCAGGGAAGAAAGGTT
-----+-----+-----+-----+-----+-----+-----+
4330          4350          4370
GTCTCCGTCTGCTGCATCGCCTTTGCCCAGCAATGAAGCCCCCAAGACAGCGGCAGCCGG
-----+-----+-----+-----+-----+-----+-----+
4390          4410          4430
TTGCCTGAACCTTCCTATCCTTGGGGGCACCCAGTGCAGGTGGATGACCCGACTCAACCT
-----+-----+-----+-----+-----+-----+-----+
4450          4470          4490
CCGCCAGGGCACCCCTCGGGGCAGGACGGGTAGCAAGGAGGGACAGAGATCGGCCCCAGG
-----+-----+-----+-----+-----+-----+-----+
4510          4530          4550
AGACCACGGAAGATCGCGCTCCTGGGGCCAACTTCAGCAGCGAGAGGCGGCCTTTGCCCA
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

[illegible][illegible]

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

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AGGCGCGGTGGTGGTGGCGGGGATGGGTTCTGCTCAGAGCTCGGGTCAGCGCGGAGGG
-----+-----+-----+-----+-----+-----+-----+
5170 5190 5210
TCTCACGGCCCCGGCACCATACGGCCAGTAGGTCAGGGCGTGGGGACTCTTTGGGGGGGT
-----+-----+-----+-----+-----+-----+-----+
5230 5250 5270
CTCCGTGGGACCTGCCCAGGGACGCTCAAGTGTGCTTGGGCTGGCCCCGGGCCGACTT
-----+-----+-----+-----+-----+-----+-----+
5290 5310 5330
GCCCACACTGCCCCGGCTGCCACTCCGCTGGCAAAGCAGAGGGCATGGCTCCCTCCCCCTC
-----+-----+-----+-----+-----+-----+-----+
5350 5370 5390
GGGGACAGCCCAGCCCCAGCCCCAGCCCATAGCCGTAGCCCCCTCTGCCTGGATTCTC
-----+-----+-----+-----+-----+-----+-----+
5410 5430 5450
GCTCTCACAACCAGCTTCCATCCGCAGGCCACCGTGTGACCCGCTCCTGCTCCTCCACCC
-----+-----+-----+-----+-----+-----+-----+
5470 5490 5510
CTTAGGACTCAGCGGGGCTCCATCCTCTAGGAAGCCCCCATGCCAAGAGTCCCCCAGAG
-----+-----+-----+-----+-----+-----+-----+
5530 5550 5570
TCCCTGCTTTGCTCTCAGGCTGCAGAACTAGCTGTGGCCTCCACCCTGCTCACCCCTCGT
-----+-----+-----+-----+-----+-----+-----+
5590 5610 5630
CCCTCCTCCCAGGGCAGCAGGGCAGTGTGTATGTTGTTTATATTGTTGCCTTGTTTGGTG
-----+-----+-----+-----+-----+-----+-----+
5650 5670 5690
AGATAGAGAAGGGCCTCTCCAGATAGAAGGTGTCTGTTTAGCAGTGCTCTGGAAAGACTG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
5710          5730          5750
CAGCTGTCTCCTCGGGGTAACCCCTCCAAACAAAGATGTTAAGATGGGGCTGGAACAACC
-----+-----+-----+-----+-----+-----+-----+

5770          5790          5810
TCTGCAAGCGGGTGGGAGGATTAGCCAGTCCTGCACAGCAAGTGCCTGGCCGGGAACAGG
-----+-----+-----+-----+-----+-----+-----+

5830          5850          5870
GAGGGCAACCAGGGAGGGGGCATGCGGGGCTGGGCTGTGCTATGCAGACTGGGCGGTGGC
-----+-----+-----+-----+-----+-----+-----+

5890          5910          5930
TTCCACAGCACTGTGTGGGGACCAACAGGTACAGGGGCCTGGTCTGTTCTGGCCCCAGG
-----+-----+-----+-----+-----+-----+-----+

5950          5970          5990
GGAGGGCCCCAGGGCGGTCCACTGCTCCCTCCCCTCTGAGCCCTATCCTGGGGTCAGGGGA
-----+-----+-----+-----+-----+-----+-----+

6010          6030          6050
GGTGATGGGACCCCTGGGAGAGGGGCGTCTATGTGCCCAATACCAGCCTGGCTCCCTCGG
-----+-----+-----+-----+-----+-----+-----+

6070          6090          6110
GTTCCACCCCATTCACCCGGTCACCGGAGCTCCAGCTCCAGCTCCAGCTCTGCCCCCTCT
-----+-----+-----+-----+-----+-----+-----+

6130          6150          6170
CTCCCTCATTGGGGTCAGGGTGCCCGTGGCCAGCACGTGCGCGCAAGGCCATGTGGACAG
-----+-----+-----+-----+-----+-----+-----+

6190          6210          6230
CACCCACACACCACACTGCACCCACACCACACCTGTGCCCGGGGCCACCCTACCTCTTCC
-----+-----+-----+-----+-----+-----+-----+

6250          6270          6290
```

FIG. 29

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```
CCAAACCCTTAGAGGCCTAGGAGCAGCAAAGCTTGGTTCTCTACTCTCAGTTAAGTGCTC
-----+-----+-----+-----+-----+-----+-----+
6310          6330          6350
TCTGGGCTGAGAGACCTCCCCTCCTTCCCCCTCCCCCACATCCACTCAGAGCCCTCCCTGC
-----+-----+-----+-----+-----+-----+-----+
6370          6390          6410
ACTGGCCCCTCTAGCCTCCTTTCCAAGGTGGCAGACTCCTCTCGGCCCTCATCTGCCTGA
-----+-----+-----+-----+-----+-----+-----+
6430          6450          6470
TGGCAATTCACTCATCCAATCAAGGAGGGCTTCTTGGAGGAAGGGTCTTTGATGTTTGTG
-----+-----+-----+-----+-----+-----+-----+
6490          6510          6530
GTCTGGGAGAGAAGGTGGAGGAGAAAAAAGGAGTTGGGGTGGCCTAGCAGGAGCTGAGTC
-----+-----+-----+-----+-----+-----+-----+
6550          6570          6590
ACTTCCACAGGCAGCCATCAGCCCAGCAGGACTGAGGCCAGGGCTGCGTGGAGGGGGGAG
-----+-----+-----+-----+-----+-----+-----+
6610          6630          6650
GCTGTCTGTTCTGGGAGCTGGGACTGGGTACCGGGGGAAGGAGGGCTGCTGCAGGCTCTG
-----+-----+-----+-----+-----+-----+-----+
6670          6690          6710
GGTGCCTGGGGCCTGGCTCCTGCAGGGCGGGCCTGTGAGAGTGGTTGGGGCCAGTGGAGG
-----+-----+-----+-----+-----+-----+-----+
6730          6750          6770
GGCTGGGAGCATTCCAGGGGAACATTCCAGGCGCCCTCTGAGTAATGCTTGGCTCTGGGA
-----+-----+-----+-----+-----+-----+-----+
6790          6810          6830
TTCCTCCTAGAGCCCCCTTAGGCACACCCGGCCAGGGAGCACCAAGGCTCCGTCCGGAAG
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

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6850 6870 6890
CGTCCCCTCCCCTTGAAGAGATGAGGAGGGGCTTCTGGGCCAGGGTACCAAACCTGC
-----+-----+-----+-----+-----+-----+-----+
6910 6930 6950
CACCAGGACAGAGTCCCCGAGGGAGCTCTGGGCAAGGTGGACCTCGCAAGGCAACATCTG
-----+-----+-----+-----+-----+-----+-----+
6970 6990 7010
GCTGTTGTTTTCTCAGATGATGGGGGGGGCACAAGTGTCTCTCTCGTACATCTCTCA
-----+-----+-----+-----+-----+-----+-----+
7030 7050 7070
CCCTAAAGGCATCTGCTGCCCATCTAAAAATCCCTAAGGCTGCCGCGCTCTTTCCTTCCC
-----+-----+-----+-----+-----+-----+-----+
7090 7110 7130
CTCTGCACTGGCGGCCTTGGCCTCTTCTTGTGATCGCCGAGCCCAAGCCTGCCCCCGA
-----+-----+-----+-----+-----+-----+-----+
7150 7170 7190
CAAAGGTCAGGGGACTCCCGTGTCCCAGCTGAGCTGTCCCTTTCAGCCTTCTCTTTTC
-----+-----+-----+-----+-----+-----+-----+
7210 7230 7250
CTCCTCCTTGATAGCTCCTCAGATCCAAGGATGCCCACGGGCGTCCCTCCTTCTCCAGGC
-----+-----+-----+-----+-----+-----+-----+
7270 7290 7310
TGAGCCACGCGTGTTGAAGGTGAAGTCTGCCCCAAAAGGCCTCCAGTGCCTCCCTGGGG
-----+-----+-----+-----+-----+-----+-----+
7330 7350 7370
ATGTCCTCTACCCCCCTCCCTCTGCTTTGTCCCATGCCCCGTGTGTTCTCAGGTCCCCCT
-----+-----+-----+-----+-----+-----+-----+
7390 7410 7430

FIG. 29

[illegible]

7450 7470 7490
GGTCCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCAGTGCCATGTC

7510 7530 7550
TCCCCGCCCTCCACAGGGGCCCTGAACCTCCCAGCCCTTTTGTCTCTCCCTACATTACAG
-----+-----+-----+-----+

7570 7590 7610
CTTCTAGTTTGTGCTGGGGTCCCCAGAACCACCAAGTCACTACTCCTATAGGCCCTGCCT
-----+-----+-----+-----+-----+

7630 7650 7670
 CCCCTGCCCTCAAGTGGGCAGAAGAAGGCACTGGGGTTTGGACATCTGGATCTCGTGAG
 -----+-----+-----+-----+-----+

7690 7710 7730
 CCCGCACACATGGAAGTCATTTTCAGCTTTCTCCACCCACCTCCCTCTTTCCCTCCCTCC
 -----+-----+-----+-----+-----+-----+

7750 7770 7790
CTGGATGATCTGGGCCACCCCCACCCCCACCAGGCAGAAATGGGTCCAGAGTTTGTGGGT

7810 7830 7850
CCTGAAGCTTTTCAGGAGCCTCTAAAAAAAAAAAAAAAAAGCACCAAAAGAAA
-----+-----+-----+-----+-----+

7870 7890 7910
CCTTTTGC AAAGTTG ACCAGAA CATGTG ACCCTGT GGCACAC TGTGTCC CTTCTC AGGG

7930 7950 7970
CCCTGCCACGAAGGCCTGAACCTTCAGCCTCACTGGCTCCTGTGGAATCCACTTCTGGTA

FIG. 29

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```
CCAGGAGGGGAAGGCTGGACACACACTGGGGTCACTCTGCCTCTGGGCCTCCCTGTCTGT
-----+-----+-----+-----+-----+-----+-----+
      8590              8610              8630
CTGGCCTGGGCTGTGACCAAGAGGAGAGCCCCAAAGGGGCTCTGCTTCCCCACCGGTGG
-----+-----+-----+-----+-----+-----+-----+
      8650              8670              8690
GCCCCTGCCCCCAGGAAGCCTGCCAAGATGGTACAGAAGAAAGAGTAGAGGCTAGGTATC
-----+-----+-----+-----+-----+-----+-----+
      8710              8730              8750
CCCTCCAAAAGGCAGGAAACACTCACATTTCAAGATGAGGGGTATATATCAAGGGGCAGG
-----+-----+-----+-----+-----+-----+-----+
      8770              8790              8810
GTACCAGGAGGGCAAGAGTAAAGATAGCAGGGGCTGCAGAGGAACAGGGACCTCGAGTAT
-----+-----+-----+-----+-----+-----+-----+
      8830              8850              8870
GGCCTTTTTCCCGGTGCAGACCTTTCCCCAATAAAGCAAGTGGCATTCCAGCCTCATGAG
-----+-----+-----+-----+-----+-----+-----+
      8890              8910              8930
CTCATGCTGGAGGCCTTGTGGGGCCTGTGGCCAGGGAGGCAAGGACCATCTGCTCCCCAC
-----+-----+-----+-----+-----+-----+-----+
      8950              8970              8990
TTGCGAAGGAAGAACTCCCTCCAAAGACTCTGAGACCCTTGGACAGGGCCCCAGGCCAGT
-----+-----+-----+-----+-----+-----+-----+
      9010              9030              9050
GCATTTTTTGGAGAAAAGGAGTCGGGGGTAAACATTCCGAAGGCGCAGCAGCCTCCCAGG
-----+-----+-----+-----+-----+-----+-----+
      9070              9090              9110
AAGCTCCTGGGCCGGCTCCAACCTCTGGGCCCCCAGCCAGGCTGAGTGGACAAGGGGGAAG
-----+-----+-----+-----+-----+-----+-----+
```

FIG. 29

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9130 9150 9170
TGGGGTGTTCACAGGGTGGGAGACGCCAAGAGGGTGGGGGAAGGAGAGAGGGCTGGCC
-----+-----+-----+-----+-----+-----+-----+
9190 9210 9230
GTCCAAGCCAGCCTCCTGACACCTAGCTGAGAGCCAGTGTGCTCTCTTGGCTGGAATGGC
-----+-----+-----+-----+-----+-----+-----+
9250 9270 9290
GTCCATGTTTACTTCGTGGGTCCAGTGAAGCAGGTGTCGGAGCCGAGGGACGGGGGGCTG
-----+-----+-----+-----+-----+-----+-----+
9310 9330 9350
CTGGAGGCCCAGGAAAACCTTTGGAAGAGGGAGCAGTTTGCCAAAATTGGAAGTGGAGGAG
-----+-----+-----+-----+-----+-----+-----+
9370 9390 9410
TCAAATTTGAATTCATAGGAAATGAGCAGCAGCTCATTTGGAACCAAGCCTCAGGTAGC
-----+-----+-----+-----+-----+-----+-----+
9430 9450 9470
AGAGGCTCTGAGGAGGCCCTGACCATGGCTACCCGATGCCCCATAATGTCCTCAGCACC
-----+-----+-----+-----+-----+-----+-----+
9490 9510 9530
CCTCTGTCTTCCCCTGCTTTTGATGCCCCTTCTGGGCATGAAAGAAGAGGGCGGGGCCAG
-----+-----+-----+-----+-----+-----+-----+
9550 9570 9590
GGGAGGGGCACCTTTCTGGGACCTCTGGTCTCTAGGGAGGATGCTGGTGTGCCTGGCAGG
-----+-----+-----+-----+-----+-----+-----+
9610 9630 9650
CTGTGCCAACGCCCTTCCAAGTGGCTGTTGTCAGGACTGCAAACATCCTGAGTTTGGGAA
-----+-----+-----+-----+-----+-----+-----+
9670 9690 9710

FIG. 29

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CATCTTTGTATGTTCTCACCTCCTCCACGCCCTCCATAGTATGTGGGGGGTCCTGCTGAC
-----+-----+-----+-----+-----+-----+-----+
9730 9750 9770
TCCCCAGCCCACGTTCTCCCCAAGAACTTCCTCCCCAGCCGGCTCCACAGGCCACCTACT
-----+-----+-----+-----+-----+-----+-----+
9790 9810 9830
CCCTGGCAGGCAGGAGGCCTGGAGGCCACCATCTCAGCTCCACACTCTTTTCTTGCCCAGG
-----+-----+-----+-----+-----+-----+-----+
9850 9870 9890
TCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTG
-----+-----+-----+-----+-----+-----+-----+
9910 9930 9950
AGCTGGAGAAGAACCAGTGAGTGCCAGGCTGGGGTAGGGCTGGGAGGAGGGGATCAGTGT
-----+-----+-----+-----+-----+-----+-----+
9970 9990 10010
TGGGGGGCAGGGACTGACACAGATCTGTGCGGGTGGCTGGATGGGCAGAGGACCCCAGAG
-----+-----+-----+-----+-----+-----+-----+
10030 10050 10070
AGGGTGCAGATGACAGGGAGAGTCACGCAGGCCTGTGGTTGGCTCCCTGGAGGCTGAAGA
-----+-----+-----+-----+-----+-----+-----+
10090 10110 10130
GGACCGCTGAGGCTGTCAGCCCCGCTGTGGGGCACCTCCGCCCTCCCAACCCCAGGAGCG
-----+-----+-----+-----+-----+-----+-----+
10150 10170 10190
GCTTGTTAGCTCCCTGCTGGCGATGAGTGAGCACCTAGTGGACATTTGCAAGATATG
-----+-----+-----+-----+-----+-----+-----+
10210 10230 10250
CTGAGTCTAAAGAAATCCTAGAGGGAAAAGATGAGCCGGCACCCCAGGCTAAGGGAATGG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
10270      10290      10310
CAGGGACCAAGATGCGGTGGCTTTGGGAGGCCGAGGCGGGCGGCTCACCTGAGGTCAGGA
-----+-----+-----+-----+-----+-----+-----+

10330      10350      10370
GTTTGAGACCAGCCTTGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAATT
-----+-----+-----+-----+-----+-----+-----+

10390      10410      10430
AGCCAGGCGTGGTGGCGGCGCCTGTAATCCCAGCTACTTAGGGGGCTGAGACGGGAGAAT
-----+-----+-----+-----+-----+-----+-----+

10450      10470      10490
CGCTTGAACCCCGAGGTAGAGGTTGTGGTGAGCCAAGATCACACCACTGCACCACTCCG
-----+-----+-----+-----+-----+-----+-----+

10510      10530      10550
GCCTGGGCAAAGAGTGAGACTCCGTCTCAAAAAAAGAGAAAAAAGAAAAAGAAAAAA
-----+-----+-----+-----+-----+-----+-----+

10570      10590      10610
AAAAGAAAGAAAGAAAAAGAAAAAGATGCAGTGGCTACACTTGGGGGCAGCAGTTTGT
-----+-----+-----+-----+-----+-----+-----+

10630      10650      10670
CTGACCTGCCTGGAAGGTCTCCATCTACAGGGAGGGGAGCAGGGGGGAATGAATTTGGAG
-----+-----+-----+-----+-----+-----+-----+

10690      10710      10730
AGTCCCAGGAGGGCCAGATCACAGAAGGCCATTTTGGTGCTCAGTGTCTTGGACCATCCA
-----+-----+-----+-----+-----+-----+-----+

10750      10770      10790
GAGCCAAAGATTTTGAGCTGGGGAAGGGACAGGCAGACCTGTGCTCAGGAAGGTGCCTTG
-----+-----+-----+-----+-----+-----+-----+

10810      10830      10850
```

FIG. 29

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GGCTGGGTGGGGTGGGTGTCCGGGCTGGAGCGCAGGCTCTTAAACCACCCAGATTATGT
-----+-----+-----+-----+-----+-----+-----+
10870 10890 10910
TATCAGTATATATCACCTACTGAGTGCTTGACCGCAGGCGCTGTTCTGAGCACTTGACAC
-----+-----+-----+-----+-----+-----+-----+
10930 10950 10970
GTATTTTATTCTCCCTCGTGGAGTCGGATGGACAGGGAACAACTCTAGTTCCACTGTGC
-----+-----+-----+-----+-----+-----+-----+
10990 11010 11030
CCAACCATATTTTCCCGACGTCCCTACCCTTTCAATGGGGTGGTCACATCACCTACCTCC
-----+-----+-----+-----+-----+-----+-----+
11050 11070 11090
TAGGGTGGCGGGTGTGTGTGGGGCAGGGGTAGGGGGCAGAGCTGGGGCAGGTGGTGGAAT
-----+-----+-----+-----+-----+-----+-----+
11110 11130 11150
GCCTGGGAGGGGGAAGCAGCCATCATTAGCGGGTGGTCTGGAGGTAATGAGGCCAAGGT
-----+-----+-----+-----+-----+-----+-----+
11170 11190 11210
GAGGTTGGGTAAAGGATTTTCTTTAAAGAAGACAGATTGACTTATGATTGATCCATCCGT
-----+-----+-----+-----+-----+-----+-----+
11230 11250 11270
GTGGGAAAGATCCTGTTGAGATGGAGCCTGAAGATGGAATCATTACCGGAGTGGGTGTGG
-----+-----+-----+-----+-----+-----+-----+
11290 11310 11330
AGAAGGCAGGGAGGGTGAAGCAGCGTGGGCAGGTGGCGATTCTGTTTTCTCTGGAGGCA
-----+-----+-----+-----+-----+-----+-----+
11350 11370 11390
GGGGGTGAGCATCAATCACTGAAGGACAGGTGGGAGGTATGTGGGGTCTAGAAGTCTGAG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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11410	11430	11450
GAAAATATTTCAAGGATCTAGGGCAGGTGGGGGCAAGAGGGTCGACCAGATGCCCAACAA		
-----+-----+-----+-----+-----+-----+-----+		
11470	11490	11510
AGGAGGGCAGCAGGCAGGGGAAGTGGGGGAGGTCACCGCATTTCCTCCCAACTCCAAGTCCC		
-----+-----+-----+-----+-----+-----+-----+		
11530	11550	11570
ATTCTTCGGCAGTGTCTCCTGACTCCTCCCTCCCGATCCTGTGGATCCTGCTGCCTGCT		
-----+-----+-----+-----+-----+-----+-----+		
11590	11610	11630
GCAGGTCCCTTGGGAACCACAACTCTTCCCTTATTCCTACTCCTCCCGGCGTCTCTCC		
-----+-----+-----+-----+-----+-----+-----+		
11650	11670	11690
TGGTGCTTCCCATATTACATCTCCCACAAGTAAAGCCATCACCAAGGCTCCTTCTCTAG		
-----+-----+-----+-----+-----+-----+-----+		
11710	11730	11750
CCCCAAGAGTTTCTGATCTGAGCAAGTCACCATGCTCCTGTCCCTTCCCTAAGACACAC		
-----+-----+-----+-----+-----+-----+-----+		
11770	11790	11810
TGTGAGTGTCTCACTCATAAAGCTGCTCCATTAGCATTTAGGGAGGAAGGCTGGGAGACA		
-----+-----+-----+-----+-----+-----+-----+		
11830	11850	11870
TCCTGGAGGAGGCAGGAGGAAGCTGAATTCACTGTTCCCTGTAAACACCCCTCTCAGCAG		
-----+-----+-----+-----+-----+-----+-----+		
11890	11910	11930
GCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCT		
-----+-----+-----+-----+-----+-----+-----+		
11950	11970	11990

FIG. 29

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GGCCCCCAACCACACGGTGAGATGCTTCCATGGGCTCTGGGATGCACCGCCAGAGGTACC
-----+-----+-----+-----+-----+-----+-----+

12010 12030 12050
CCCCCACCATTCCCTACCCCTACTCCTCCTTGCATTCCCTAAGGGGCGGTTGGAGCCAGCCC
-----+-----+-----+-----+-----+-----+-----+

12070 12090 12110
CTACCACACCCTCCCTCTTGCCCTCTTGCTCCAGCCCTGGCTGAGATTGGGGCTGGCC
-----+-----+-----+-----+-----+-----+-----+

12130 12150 12170
CCTTCCTCCCTAGGATCATTTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTG
-----+-----+-----+-----+-----+-----+-----+

12190 12210 12230
GGTAGTCCTCTGCACCTGCTCTGGGATGAGGTGAGCTCTGGGAGAGGAGGCTGGGCCTGG
-----+-----+-----+-----+-----+-----+-----+

12250 12270 12290
GATGGGGAAAGAGCTCCCTCACACCCGCTCCTACCCCTCTGCACCCTAGTGGCCTGATCA
-----+-----+-----+-----+-----+-----+-----+

12310 12330 12350
CCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACT
-----+-----+-----+-----+-----+-----+-----+

12370 12390 12410
TCTCAACCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCC
-----+-----+-----+-----+-----+-----+-----+

12430 12450 12470
ACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGAGCAGGG
-----+-----+-----+-----+-----+-----+-----+

12490 12510 12530
TCAGGGGCATCGATCGGATGGGAGTGGGAATGCTGTATCTATAGCCCTCCAAATCAGAAG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
12550      12570      12590
AGACAGGAATTACAGGCCTCGAGTCCCAGTATTTTATTGAAGTCTGAAGAAACAAGTT
-----+-----+-----+-----+-----+-----+-----+

12610      12630      12650
CCAGAAAACATGTAAACTTCCTTCTGGGAGCTGGGGTTGGGGGTCAGGGCTCAAGCCCA
-----+-----+-----+-----+-----+-----+-----+

12670      12690      12710
GCAGCTTCCACTCAGGGTCCCCATTTGCACCTCCGCAGGGCAGGCGAGAAGCGCGCAGGA
-----+-----+-----+-----+-----+-----+-----+

12730      12750      12770
CCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTGGTGAGGAGAGACCCCA
-----+-----+-----+-----+-----+-----+-----+

12790      12810      12830
GGGGTTGGCGGGGTCAGGGATGGGGCCAGCTCAGCCCCTCAAGCCACCGGGATTTCTGCC
-----+-----+-----+-----+-----+-----+-----+

12850      12870      12890
TTCCCAGTTCTTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGT
-----+-----+-----+-----+-----+-----+-----+

12910      12930      12950
CGCCAACTACGTGGACCAGGTTGGGGGCGGCGGGGAGAGAGCGGTGATGGGGGTGGCGGC
-----+-----+-----+-----+-----+-----+-----+

12970      12990      13010
GGCAGGACAGGCAGGTGCTGCTGGTGGGGTTTGGGGAAGAGGAAGGGCGCCCCACGAAGGACC
-----+-----+-----+-----+-----+-----+-----+

13030      13050      13070
ACCGGCGCGATGGGGCGCCCTGTCCCGGCTTCAGCCCCGCCTCGCCCTCAGCTTCTCAGG
-----+-----+-----+-----+-----+-----+-----+

13090      13110      13130
```

FIG. 29

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ACTCTGGACATTTCAGGTGGCGCTGACCGGCCTGGAGGTGTGGACCGAGCGGGACCGCAGC
-----+-----+-----+-----+-----+-----+

13150 13170 13190
CGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTG
-----+-----+-----+-----+-----+-----+

13210 13230 13250
TGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGTGGGTGCCCTCTGACCCGGACG
-----+-----+-----+-----+-----+-----+

13270 13290 13310
CGGGTCCCGGTGGGGCGGCCTCACCTCCCGGCCCCGCCTGGTCACGCCGCGCTCCGCCC
-----+-----+-----+-----+-----+-----+

13330 13350 13370
CCAGGGGCCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCATGTGCC
-----+-----+-----+-----+-----+-----+

13390 13410 13430
GCGCCGAGAGCTCGGGAGGCGTGAGCACGGTGAGCCCCGCGGGCGGGGGCGAGGGAGAGA
-----+-----+-----+-----+-----+-----+

13450 13470 13490
CAGGAGGCTCTACGGCCGAGTGACCGCCCTCCACGGCCCCCAGGACCACTCGGAGCT
-----+-----+-----+-----+-----+-----+

13510 13530 13550
CCCCATCGGCGCCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCA
-----+-----+-----+-----+-----+-----+

13570 13590 13610
CGACCCCGACGGCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGC
-----+-----+-----+-----+-----+-----+

13630 13650 13670
GGCCACCGGGTACGCGGGTGGGGGGTGGGGGCTGCGGCGGGGCGGCTAGTCCTGGGGACT
-----+-----+-----+-----+-----+-----+

FIG. 29

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```
13690      13710      13730
TCCTCCGCTGCGTTTCTTTGGTCGTCCTCAGTTTCCTCTTCTGTAAAATGGGGATAATG
-----+-----+-----+-----+-----+-----+-----+

13750      13770      13790
ATCATAGTGTCCGCTTCAGGGTGGTTTATGAGGCTTAAAGGGAAGAAGCTCAGGCAAAGT
-----+-----+-----+-----+-----+-----+-----+

13810      13830      13850
GGATTCTCAACGGTATGAAGATTATTTTCCGAGTAACCTGGCGAGGTTACTCCTACACCG
-----+-----+-----+-----+-----+-----+-----+

13870      13890      13910
GGAGGAGCACCGTCGGGTCGCGATTCCACCTTGGGTCCCGGGCTGCTCACTATTGGGGCC
-----+-----+-----+-----+-----+-----+-----+

13930      13950      13970
GCATCGTCCCCTGTCCCGCTTGTGTGTGACTTTGCGCGGGTTACTTCCCCTCTCTGGGC
-----+-----+-----+-----+-----+-----+-----+

13990      14010      14030
TCTGCGCGTCTGGCGGCTGTAGCCAAGCCCAGGGGTGGGGATCAGAGAAGCGCGGGGGTT
-----+-----+-----+-----+-----+-----+-----+

14050      14070      14090
GGGGGACTGTCCCTCCATGCCCAATGCCCTCCCCGTGCCGGTAGGCACCCGTTTCCGCGC
-----+-----+-----+-----+-----+-----+-----+

14110      14130      14150
GTGTTTCAGCGCCTGCAGCCGCCCGCAGCTGCGCGCTTCTTCCGCAAGGGGGCGGCGCT
-----+-----+-----+-----+-----+-----+-----+

14170      14190      14210
TGCCTCTCCAATGCCCCGGACCCCGACTCCCGGTGCCGCCGGCGCTCTGCGGGAACGGC
-----+-----+-----+-----+-----+-----+-----+

14230      14250      14270
```

FIG. 29

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```
TTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGTTAAGTCGGCTCGCCCCG
-----+-----+-----+-----+-----+-----+-----+
14290              14310              14330
GCCCCCACTTGCCCTCTCCGCTCAGGTCTGGGGCGCTGCGCCCTCACCTGGGCCCCTTCTT
-----+-----+-----+-----+-----+-----+
14350              14370              14390
GCCTTTCTGGTCCCAGGAGTGCCGCGACCTCTGCTGCTTTGCTCACAACTGCTCGCTGCG
-----+-----+-----+-----+-----+-----+
14410              14430              14450
CCCGGGGGCCAGTGCGCCACGGGGACTGCTGCGTGCGCTGCCTGGTGAGGGCATGGAA
-----+-----+-----+-----+-----+-----+
14470              14490              14510
GGTTCAGGGTGAGGGTTTCGGGGAGCTTGGGAGCCGGCCTGTTGGCCTTAGTTAATTGGT
-----+-----+-----+-----+-----+-----+
14530              14550              14570
GCCCTCAGGTTCCCCCGTTGGGTGCTGGGCTTGGGTAGGCCTGGCTCCCCCAGCTCCGAG
-----+-----+-----+-----+-----+-----+
14590              14610              14630
CCGCGCTCTCGGCATGGACCTCTCACTGCACGTGGCCTCTCTCTGCCTTCCCCACCAACC
-----+-----+-----+-----+-----+-----+
14650              14670              14690
GTCACCTGCGCAGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGA
-----+-----+-----+-----+-----+-----+
14710              14730              14750
CCTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTACCTACTGGA
-----+-----+-----+-----+-----+-----+
14770              14790              14810
CGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGA
-----+-----+-----+-----+-----+-----+
```

FIG. 29

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```
14830      14850      14870
GCAGCAGTGCCAGCAGCTCTGGGGGCTGGTGAGAGGACACGAGCACCCCTTGCACCCTGC
-----+-----+-----+-----+-----+-----+-----+

14890      14910      14930
CCCCCATCCTCTGGTGGGGCCAGTTTCTACTGTGGGGAAGATGGGCAGGGGAACTGAG
-----+-----+-----+-----+-----+-----+-----+

14950      14970      14990
GCCCCGTGAGCGCAGCCCCCTCTCCGAGCTGCCCCAGCCTGGCCCATGCTTCCTCAGGCT
-----+-----+-----+-----+-----+-----+-----+

15010      15030      15050
CCCCCCCAGCTCCCGAGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAA
-----+-----+-----+-----+-----+-----+-----+

15070      15090      15110
ACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGCTAGGGAGTGGAGC
-----+-----+-----+-----+-----+-----+-----+

15130      15150      15170
TGAGTGGAGGGAGCAGAAGCTATGGAGTGGGTTTGGGGAAGGGGGGTACTGCAGCTGTTG
-----+-----+-----+-----+-----+-----+-----+

15190      15210      15230
ACCCCCCTCTACTTCCTCCCCAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGGA
-----+-----+-----+-----+-----+-----+-----+

15250      15270      15290
AAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGC
-----+-----+-----+-----+-----+-----+-----+

15310      15330      15350
CAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGG
-----+-----+-----+-----+-----+-----+-----+

15370      15390      15410
```

FIG. 29

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CTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGAGCTCTGCCCACCCG
-----+-----+-----+-----+-----+-----+-----+
15430 15450 15470
ACCCCTCCTTGCCGTTTGAATCCCGCAGGCCAGTGTCCCCCTCACTGCCTGGTGCATGC
-----+-----+-----+-----+-----+-----+-----+
15490 15510 15530
CCGTAGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGC
-----+-----+-----+-----+-----+-----+-----+
15550 15570 15590
CTGACTGCCTGCCACAGCCACGGGGTGAGAGCCCGAGGAGTGGGGGTGACCTTGGGGTTC
-----+-----+-----+-----+-----+-----+-----+
15610 15630 15650
CTAATCCTACGTGACCCTCCTCTTCTCTTCTCTGCAGGTTTGCAATAGCAACCATAACTG
-----+-----+-----+-----+-----+-----+-----+
15670 15690 15710
CCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCAT
-----+-----+-----+-----+-----+-----+-----+
15730 15750 15770
GGACAGTGGCCCTGTGCAGGCTGAAAGTATGCCAGTGGGGGGCATGTGGGCAGGAGCTGG
-----+-----+-----+-----+-----+-----+-----+
15790 15810 15830
GGTGGTGCACCTGCTCAGGACTCAGCGCCCCTTCCCCCAATCCCCGCAGACCATGACACC
-----+-----+-----+-----+-----+-----+-----+
15850 15870 15890
TTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGGGGGCCGCCTGGCC
-----+-----+-----+-----+-----+-----+-----+
15910 15930 15950
TGGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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15970	15990	16010
GACCCTGCGTGCACTGGGTAGGCTCCGAGCGCCTGCTTCCTGAGCCTACTCCTGCGGTTC		
-----+-----+-----+-----+-----+-----+-----+		
16030	16050	16070
CCCTCCTCAGAGCTCTGCTGGGGCTGTGGGAGCTGGGGCAGGCCCTCAGCCTTGCCCCCA		
-----+-----+-----+-----+-----+-----+-----+		
16090	16110	16130
GGTGCAGAGAGCAGCCCCAGAGGCCATGGAAAGAAGTAGCTTTGAACAGGAGGTTCCAGT		
-----+-----+-----+-----+-----+-----+-----+		
16150	16170	16190
GGCCTCCCAGTCAAGCGAGGGGGTGGATCCCTGCCCCACCACCAGCACCGCAAGGCATGG		
-----+-----+-----+-----+-----+-----+-----+		
16210	16230	16250
CCCTCTACCTCCCAGTACAGCTCCTCTTGCTCCACTCTCCTGCTTCTCCCACCAGCTGGCT		
-----+-----+-----+-----+-----+-----+-----+		
16270	16290	16310
GCCTCACCTTGACTTCGCCCTGTTTTTCCCTGGCTCAGATTGCAGTCCCTGTACCATGC		
-----+-----+-----+-----+-----+-----+-----+		
16330	16350	16370
TGCCCCCGGAGGCCTGTCCAGCCTCTGTCTCACCAGTTTTTGGGCCCTTTGCCACTTCCTC		
-----+-----+-----+-----+-----+-----+-----+		
16390	16410	16430
TGCACAAATCACCTCTGTCACCCCTTGAAGTTCCCAAATGCTGGGGCCAGCACATCTTT		
-----+-----+-----+-----+-----+-----+-----+		
16450	16470	16490
TCACTCCATACCACTGGTCAGCTGCGGTGCTGGCTGCCCCTGTGCCAGGGCCCTGCCTTA		
-----+-----+-----+-----+-----+-----+-----+		
16510	16530	16550

FIG. 29

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ACCCAGTTCTCTGTGACCTGGGTGGTGGCGGAGTGGGGAGTCACATAATACTAAGCATGG
-----+-----+-----+-----+-----+-----+-----+
16570 16590 16610
CTGTCTAGGACTCACCTGCACCAGGGCCCTAGGCAGGGCAGGCACCTCTGTGGCCATGT
-----+-----+-----+-----+-----+-----+-----+
16630 16650 16670
CTGACATAGCCTGGTCTTGGGAGTGCTCCGGGCAAGCCAAGGGAGATGGCATGATTTGGG
-----+-----+-----+-----+-----+-----+-----+
16690 16710 16730
CCAGAGATGGGGGCAGAGGGCATAACAGACAGGGGCAGGGCACCACCTGGGCCCCGGGTG
-----+-----+-----+-----+-----+-----+-----+
16750 16770 16790
GCAGCTAAGAGGACCCTGACAAAGCGAGTTGTGATTGAGGGTCTGTGGGCAGAGGAGCAA
-----+-----+-----+-----+-----+-----+-----+
16810 16830 16850
GGTGGCCAGAGCCTGGCGTGTGACACGGAGGGGGCGCTGCAGAGGGTGGCGGCTGCTTC
-----+-----+-----+-----+-----+-----+-----+
16870 16890 16910
TCATCCCCAGGCGGGAGTCTCAGGGCAGGGGAGAATGTTTTGAAGGAACATCACAGGAAA
-----+-----+-----+-----+-----+-----+-----+
16930 16950 16970
TGACAAGGCCTTGGGGGATGGGATGGGGACAGTCAAAGATGGCTTGAATCATCAAGGGC
-----+-----+-----+-----+-----+-----+-----+
16990 17010 17030
AGCAGGGCAGCCAGGGGCAAGGAGAGCAGACATAGCTGCCGAAGGGGCGGACATCCAAGG
-----+-----+-----+-----+-----+-----+-----+
17050 17070 17090
TTCTTTGGAAGCTGAGCGATGCCAGCATCTGGAGAGTGCCAGGCTGCTGGGTGGTGTGAG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

Variable	Mean	Standard deviation	Minimum	Maximum
Age	35.2	10.5	20	55
Gender	0.52	0.50	0	1
Marital status	0.68	0.48	0	1
Education	12.5	2.1	9	16
Income	15.2	3.5	10	25
Health status	0.75	0.43	0	1
Employment status	0.82	0.38	0	1
Home ownership	0.91	0.29	0	1
Vehicle ownership	0.78	0.41	0	1
Life satisfaction	4.2	1.8	1	7
Subjective health	3.8	1.5	1	6
Life expectancy	78.5	5.2	65	90
Quality of life	5.1	2.2	1	9
Healthcare access	0.85	0.35	0	1
Health insurance	0.95	0.22	0	1
Healthcare costs	12.8	4.5	5	25
Healthcare quality	4.5	1.2	1	6
Healthcare satisfaction	4.8	1.5	1	6
Healthcare accessibility	4.2	1.8	1	6
Healthcare affordability	4.0	1.6	1	6
Healthcare effectiveness	4.3	1.7	1	6
Healthcare safety	4.6	1.4	1	6
Healthcare equity	4.1	1.9	1	6
Healthcare transparency	4.4	1.6	1	6
Healthcare accountability	4.7	1.3	1	6
Healthcare responsiveness	4.9	1.1	1	6
Healthcare patient-centeredness	5.0	1.0	1	6
Healthcare cultural competence	4.8	1.2	1	6
Healthcare community engagement	4.6	1.4	1	6
Healthcare leadership	4.5	1.3	1	6
Healthcare governance	4.4	1.2	1	6
Healthcare innovation	4.3	1.1	1	6
Healthcare research	4.2	1.0	1	6
Healthcare education	4.1	0.9	1	6
Healthcare workforce	4.0	0.8	1	6
Healthcare infrastructure	3.9	0.7	1	6
Healthcare information technology	3.8	0.6	1	6
Healthcare data management	3.7	0.5	1	6
Healthcare quality improvement	3.6	0.4	1	6
Healthcare patient safety	3.5	0.3	1	6
Healthcare infection control	3.4	0.2	1	6
Healthcare accreditation	3.3	0.1	1	6
Healthcare certification	3.2	0.1	1	6
Healthcare licensure	3.1	0.1	1	6
Healthcare regulation	3.0	0.1	1	6
Healthcare policy	2.9	0.1	1	6
Healthcare legislation	2.8	0.1	1	6
Healthcare executive order	2.7	0.1	1	6
Healthcare court decision	2.6	0.1	1	6
Healthcare administrative action	2.5	0.1	1	6
Healthcare public health	2.4	0.1	1	6
Healthcare epidemiology	2.3	0.1	1	6
Healthcare biostatistics	2.2	0.1	1	6
Healthcare clinical research	2.1	0.1	1	6
Healthcare behavioral research	2.0	0.1	1	6
Healthcare social research	1.9	0.1	1	6
Healthcare environmental research	1.8	0.1	1	6
Healthcare policy research	1.7	0.1	1	6
Healthcare evaluation research	1.6	0.1	1	6
Healthcare implementation research	1.5	0.1	1	6
Healthcare dissemination research	1.4	0.1	1	6
Healthcare knowledge translation	1.3	0.1	1	6
Healthcare patient engagement	1.2	0.1	1	6
Healthcare community participation	1.1	0.1	1	6
Healthcare patient empowerment	1.0	0.1	1	6
Healthcare patient education	0.9	0.1	1	6
Healthcare patient counseling	0.8	0.1	1	6
Healthcare patient support	0.7	0.1	1	6
Healthcare patient advocacy	0.6	0.1	1	6
Healthcare patient representation	0.5	0.1	1	6
Healthcare patient voice	0.4	0.1	1	6
Healthcare patient choice	0.3	0.1	1	6
Healthcare patient control	0.2	0.1	1	6
Healthcare patient autonomy	0.1	0.1	1	6

FIG. 29

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CCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGGTAGGCAGG
-----+-----+-----+-----+-----+-----+-----+
17710 17730 17750
GACCTGGATTCAAAGCCTCCCCCTCTCATCGCCACCCCTCCCACCTCTCCCACCCCTCAG
-----+-----+-----+-----+-----+-----+-----+
17770 17790 17810
TTTGCTGCCCCCTAATCAGGTTTCTGGGCTCAGGTTATTATGGAAATGAGTTTATGACCT
-----+-----+-----+-----+-----+-----+-----+
17830 17850 17870
CTTGCTTATCATGGAGACCAGGATGCTGGAAGCCCTGGGCTGGGGAGGGAGAAGCTGTG
-----+-----+-----+-----+-----+-----+-----+
17890 17910 17930
GCTTTTCTGGATCACTGGTCTCACTGAGTGAGGATGGGCTCTCTGCCACACAGCTTGC
-----+-----+-----+-----+-----+-----+-----+
17950 17970 17990
AGCCTGGGGCCCCAGTCCCTTAGGGGACAACATATCCTCCTCATTCTCAGCAGATCAAGTC
-----+-----+-----+-----+-----+-----+-----+
18010 18030 18050
CAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGAC
-----+-----+-----+-----+-----+-----+-----+
18070 18090 18110
AGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTGCAGGGGCAGAGCCAGTGAATCAC
-----+-----+-----+-----+-----+-----+-----+
18130 18150 18170
CGGACCTCCAGCACCTGCAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCA
-----+-----+-----+-----+-----+-----+-----+
18190 18210 18230
CCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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```
18250      18270      18290
CACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCCTGACC
-----+-----+-----+-----+-----+-----+-----+

18310      18330      18350
TCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAAGGGCTCTGTCCTGGGAGT
-----+-----+-----+-----+-----+-----+-----+

18370      18390      18410
CTGGTGTGTCTCCTACATGCAATTTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTG
-----+-----+-----+-----+-----+-----+-----+

18430      18450      18470
GCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTTCGACTGAGTCCACACTCCCCTGAGCC
-----+-----+-----+-----+-----+-----+-----+

18490      18510      18530
TGGCTGGCCTCTGCAAACAAACATAATTTGGGGACCTTCCTTCCTGTTTCTTCCCACCC
-----+-----+-----+-----+-----+-----+-----+

18550      18570      18590
TGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCCACCCCAATCCCAGTGCTACACCTGAGG
-----+-----+-----+-----+-----+-----+-----+

18610      18630      18650
TTCTGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTGTCGGGGGGACAGAGG
-----+-----+-----+-----+-----+-----+-----+

18670      18690      18710
GAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGC
-----+-----+-----+-----+-----+-----+-----+

18730      18750      18770
GTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGGATCACCAGA
-----+-----+-----+-----+-----+-----+-----+

18790      18810      18830
```

FIG. 29

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GGCCAGCAGGTCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATT
-----+-----+-----+-----+-----+-----+-----+
18850 18870 18890
TTAAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAG
-----+-----+-----+-----+-----+-----+-----+
18910 18930 18950
CAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCAC
-----+-----+-----+-----+-----+-----+-----+
18970 18990 19010
TCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAATTTTAAAAAGACATATTA
-----+-----+-----+-----+-----+-----+-----+
19030 19050 19070
ACTTGACCTTGGTTAGTCTTTTCTGTATGTAAATTCAACCCATGGGGTGCCCTGAGGAC
-----+-----+-----+-----+-----+-----+-----+
19090 19110 19130
CCACACGGGGTGGTGGTTGGCGGGTGGTGGTTGGTGGGGTGGTGGCTGACGGGGTGGTG
-----+-----+-----+-----+-----+-----+-----+
19150 19170 19190
GCTGGCAGGCCGAGCCTAGATGGCAGCCAGAGCCCCAGGCATGTGTCTGGGCACAGGACG
-----+-----+-----+-----+-----+-----+-----+
19210 19230 19250
GTGTTGCCTAGTTTGAACACCCTCTTTGCTCTGTCACTCCTGCCTCCCTTGGGCGTTTAC
-----+-----+-----+-----+-----+-----+-----+
19270 19290 19310
ATTCTCCCATTTGCTTCATGCAAGAGCTGCTGAGTGGCCTATATCAGCCAGCTGTTGCCGC
-----+-----+-----+-----+-----+-----+-----+
19330 19350 19370
ATAACAAAACCATCCCAAACTGAGTGCAGGGAGGCAACTTCACCTCGGGCTCCACTCCA

FIG. 29

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```

-----+-----+-----+-----+-----+-----+
      19390              19410              19430
      .               .               .
CAAGCCCAAGGGGCCAGGTGAGAGTGCTCTCTAAAGCCCCCTCCTGCCTCAGTTGTAGTT
-----+-----+-----+-----+-----+-----+

      19450              19470              19490
      .               .               .
GCAAAATTTTAATTTATGAAGGTGACTGATGACACAGAGGCCAATGCTGTTGAAATAAGT
-----+-----+-----+-----+-----+-----+

      19510              19530              19550
      .               .               .
TATTACTCACAGTTTCCCACCATGCAGGGCCACAGTGGGGAGGCCACTAGGTTTGGTCCAG
-----+-----+-----+-----+-----+-----+

      19570              19590              19610
      .               .               .
GGACAGAATCAGGAGCGAGTGGAAGGCACAGGCCACAGCCCACAGTGCCGTTTCCACTGG
-----+-----+-----+-----+-----+-----+

      19630              19650              19670
      .               .               .
GGAGGCAAGGCAGGCCAGGGGAAGAGGGTAGGATTGGCATTTTGAATCATTCTGGTGGGG
-----+-----+-----+-----+-----+-----+

      19690              19710              19730
      .               .               .
TTTGGGGCGTGCGGTTGGGCTCTAATTGTCTGGGTAGGTGCCTGGCCCTGAGCTGGTTTA
-----+-----+-----+-----+-----+-----+

      19750              19770              19790
      .               .               .
GGGCAGGGGAAATACTGGTTTCGTATGTGAGAGTTCCTTGAAGGGGGTGGTTGGTGTATG
-----+-----+-----+-----+-----+-----+

      19810              19830              19850
      .               .               .
GACTCAAGACTGGTCGGTTTGCATATGAAAGGCATGAGTTGTTTCTGATCTCCAGGAATC
-----+-----+-----+-----+-----+-----+

      19870              19890              19910
      .               .               .
AAGCAGTTTCTCTCCAGCCAACAAGCCCCCAGATGTTAAACCATCATAAAATAG
-----+-----+-----+-----+-----+-----+

```

FIG. 29

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```
19930          19950          19970
.
AGAATCTAAGGCCAGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAG
-----+-----+-----+-----+-----+-----+-----+
19990          20010          20030
.
GCGGGAGGATCATTGAGGTGAGAAGTTCGAGACCAGCCTGGCCAATGTGGTGAAACCCC
-----+-----+-----+-----+-----+-----+-----+
20050          20070          20090
.
ATCTCTACTAAAAATACAAAAATTAGCCCGGTGTGGTGGCACGTGCCTATAATCCCAGCT
-----+-----+-----+-----+-----+-----+-----+
20110          20130          20150
.
ACTCGGGAGGCTGCGGCAGGAGAATTGTTTGAACATGGGAGGTGGAGGTTGCAGTGAGCT
-----+-----+-----+-----+-----+-----+-----+
20170          20190          20210
.
GAGATCGTGCCACTGCACTCCAGCCTGGGCAACAAGAGCAAGACTCCGTCTCAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+
20230          20250          20270
.
AAAAAAAAAAAAAGAGAGACTCTAAAAATACACGTTAATATACCTCCCCCGCTCTTACCCT
-----+-----+-----+-----+-----+-----+-----+
20290          20310          20330
.
TCAGGAGGGGGTGTCTAGACCCCGCGGACTCCAGCTACAAGGGACCCTGGGGAGGCCAA
-----+-----+-----+-----+-----+-----+-----+
20350          20370          20390
.
CTCTGCCCTCTTGGCTAATCCCCAAGACTGCCAGCACCCCTCCACCCCTTCTCCATTC
-----+-----+-----+-----+-----+-----+-----+
20410          20430          20450
.
AGTGGCGAACCTTGGGGAGGCCACGTGGGAAGGAAAGAGGGCTCTAAGAGGGGAGGCCCC
-----+-----+-----+-----+-----+-----+-----+
20470          20490          20510
.
AGACTGGGGGAGAGGCCTGTCTGGAGCCCAGGATCACCTGGCTGTGCTGCAGAACTGGAG
```

FIG. 29

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```
-----+-----+-----+-----+-----+-----+
      20530              20550              20570
AAGAGAAGCTCAGCAGAAAGGAGCTGGCATGGGGCCAACAGCAGAAAAGCAGGAGGCACG
-----+-----+-----+-----+-----+-----+

      20590              20610              20630
CAGAAGTGACTGGGAAGCAGGAGGGTAGGCATGGACCCTGAGGCTGAGCAGGAGGTACTG
-----+-----+-----+-----+-----+-----+

      20650              20670              20690
AGGGGCAGAGTGGACGCTGAGCTGGGGGTAGCGAGCGAGCCCAGCTCAGCTGTGACGCCC
-----+-----+-----+-----+-----+-----+

      20710              20730              20750
TCTGTTTGGCCACCCAACCTACCAGCTACTTGGGCTGCCCCGGGAGGAACTGGGCTTCCTC
-----+-----+-----+-----+-----+-----+

      20770              20790              20810
TGACATTCTGTGGCCTGCGGCCATCTGTGCACACCTTCTTCTCTCTGCCCCCTCCCTTGA
-----+-----+-----+-----+-----+-----+

      20830              20850              20870
CTTGTGGCACCCACAGACAGGTGGGAGAGTGTACCTGCCCTGTGTGGTCAGAGCTTGGTT
-----+-----+-----+-----+-----+-----+

      20890              20910              20930
TTGAGTTTCCTTCCCTCACCCCTCTTTCCTCCACACGCCAAAACACAAGAGGATGTGTC
-----+-----+-----+-----+-----+-----+

      20950              20970              20990
AGAGGCCTGTGAACCAGAGCAACTCCATCCTGAATAGGGGCTGAGCAAAATAAGGCTGAG
-----+-----+-----+-----+-----+-----+

      21010              21030              21050
ACCTACTGGGCTGCGTTTCCAGACAGTTACAGCATTCTGCGTCACAGGATGAGATAGGAG
-----+-----+-----+-----+-----+-----+
```

FIG. 29

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```
21070      21090      21110
ATACAGGTCATAAAGACCTTGCTGATAAAATAGTTTGCAGTAGGCCAGGCGCGGTAGCTC
-----+-----+-----+-----+-----+-----+-----+

21130      21150      21170
ACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCGGATCACCTGAGGTCAGAAGT
-----+-----+-----+-----+-----+-----+-----+

21190      21210      21230
TCGAGACCAGCCTGGCCAACAAGGTGAAACCTCATCTCTACTAAAAATACAAAACTAGC
-----+-----+-----+-----+-----+-----+-----+

21250      21270      21290
CAGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG
-----+-----+-----+-----+-----+-----+-----+

21310      21330      21350
CTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCTGAGATCATGTCACTGCACTCCAGCCTG
-----+-----+-----+-----+-----+-----+-----+

21370      21390      21410
GAGCGAGACTCCGTCTCAAAAACCAAACCAACCAAAAAAATCAGCTTGCAATATAGAAGC
-----+-----+-----+-----+-----+-----+-----+

21430      21450      21470
TGGCTAAACCCACCCAAACCAAGATGGTGATGAGAGTGACCTCTGGTCGGTCCCCACTG
-----+-----+-----+-----+-----+-----+-----+

21490      21510      21530
CTACACTCCCACCAGCACCATGACAGGTTACAGATGCCATGGCAGTATCAGGAAGTTACC
-----+-----+-----+-----+-----+-----+-----+

21550      21570      21590
ATATATGGTCTAAAAAGGGGAGACATGAACAATCCACCCCTGTTTAGCAGATCATCCAGA
-----+-----+-----+-----+-----+-----+-----+

21610      21630      21650
AACAACCATAAAAAATGGGCAACCAGCAGCCCTCAGGGCTGCGCTCTCTATGGAGTAGCCA
```

FIG. 29

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```
-----+-----+-----+-----+-----+-----+
      21670              21690              21710
      .               .               .
TTCTTTTATTCTTTTACTTTCTTAATAAAATGTGCTTTCACTTTATGGACTCGTCTCAAAT
      .               .               .
-----+-----+-----+-----+-----+-----+

      21730              21750              21770
      .               .               .
TCTTTCTTGCACGAGATCCAAGAACCCTCTCCTGGGGTCTGAATCTGGACCCCTTTCCGG
      .               .               .
-----+-----+-----+-----+-----+-----+

      21790              21810              21830
      .               .               .
TAACAGATGTCGTAGAGTGAAGCACAAACCACTGCAGGGGCATCTTGGTTTACATTTTGCT
      .               .               .
-----+-----+-----+-----+-----+-----+

      21850              21870              21890
      .               .               .
TCAGCGGCCATGGTTAGCACAGCGGAAAGCACATCACAGTCTTCTGATTCATTAAAAAAA
      .               .               .
-----+-----+-----+-----+-----+-----+

      21910              21930              21950
      .               .               .
TTAGGAAATGGACCACCACAAACCACAGACAGATGTACTGAGACAGGATAGGTAGTCAAG
      .               .               .
-----+-----+-----+-----+-----+-----+

      21970              21990              22010
      .               .               .
AAAGTGACCATGTTCTAGGCGCGCAGCAGCAACTGTGGTGACCGTACAGTCAACAAGCCT
      .               .               .
-----+-----+-----+-----+-----+-----+

      22030              22050              22070
      .               .               .
CAGCACTGGCATTGCAATTGAGCTCATTCAAGCAAAGCTATCTTCAGCAGGGACTTCTCC
      .               .               .
-----+-----+-----+-----+-----+-----+

      22090              22110              22130
      .               .               .
CTCTAGGCAGCAAGCGCATTTTTATTTTACCTGTCCTCAAAGTATCCTTTGCTCCTTAT
      .               .               .
-----+-----+-----+-----+-----+-----+

      22150              22170              22190
      .               .               .
AACAGTAAGGAACACACCCCTGTGTGGAGATTTAAGATGCTAATGAGGCCAAGCGCAGTT
      .               .               .
-----+-----+-----+-----+-----+-----+
```

FIG. 29

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22210	22230	22250
GCTCACGTCTGTAATTCCAGCACTTTGGGAGGCAGAGGTGGGCGGGTCACCTTGAGGTTAG		
-----+-----+-----+-----+-----+-----+-----+		
22270	22290	22310
AAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTACTAAAAATACAAAAAT		
-----+-----+-----+-----+-----+-----+-----+		
22330	22350	22370
TAGCCGGGCATGGTGGCGGGCGTCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGAAGA		
-----+-----+-----+-----+-----+-----+-----+		
22390	22410	22430
ATCGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAG		
-----+-----+-----+-----+-----+-----+-----+		
22450	22470	22490
CCTGAGGGAGAGAGAGAGCAAGACATCGTTTTTGTGTTGTTGTTGTTGTTGTTGTTGTT		
-----+-----+-----+-----+-----+-----+-----+		
22510	22530	22550
TTTTAAAAAAGTCAAGACAAATCATAGTGGGGGCTTTTCTGGTCACTTTTAAATCTT		
-----+-----+-----+-----+-----+-----+-----+		
22570	22590	22610
AGTGTTGAGACTTTATTTGAGACAGGGCCTTACTCTGTTGCCAGGTTGGATGAGATTTT		
-----+-----+-----+-----+-----+-----+-----+		
22630	22650	22670
TAACCTCAATATTTACTTATAGAATAACTTTTTGGTTAGTCAAAACAATGCTGTGTCTCA		
-----+-----+-----+-----+-----+-----+-----+		
22690	22710	22730
TTCTGATCAGAATAAAACATCAGACAACCTCAAGAGAAACATTCTGCAAAATAACTGGCCA		
-----+-----+-----+-----+-----+-----+-----+		
22750	22770	22790
GGATTCTTCAAAAGTGTCAAGGGTAAAGATAAGGAAAGATGAAGGAACCTCCAGATTGAG		

FIG. 29

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```
-----+-----+-----+-----+-----+-----+
      22810              22830              22850
      .               .               .
GAGAATAAGGAGACAAC.TGTGATGTGGGATCCTAGAAATGGATCTTGGAAACAGAAAAAGGA
-----+-----+-----+-----+-----+-----+

      22870              22890              22910
      .               .               .
CATTAGTGGAAAAATGAGAAATGCAAAACAGTCTACAGTTTCGTTAACAGGATTGTACCA
-----+-----+-----+-----+-----+-----+

      22930              22950              22970
      .               .               .
AGGTTAGTTTCCTAGCTGTAATGATTGGACTATGATTAAGTAAGATGGACCATCAGGGGA
-----+-----+-----+-----+-----+-----+

      22990              23010              23030
      .               .               .
AGCTGGGTGAAGGGTGTAAGGAAAATGCTTACATTTTCCAACCTTTCTGCAAGTCTAAAA
-----+-----+-----+-----+-----+-----+

      23050              23070              23090
      .               .               .
TTAGTCAACAATAAGAAGTTTAAATAGGCCAGGCATGGTGGCTCACACCTGTCATCCTA
-----+-----+-----+-----+-----+-----+

      23110              23130              23150
      .               .               .
GCAC'TTTGAGAGGCCGAGGTGGGAGGATGGTTTGAGCCCAGGAGTTCAAGACCAGCCTGC
-----+-----+-----+-----+-----+-----+

      23170              23190              23210
      .               .               .
GCAATAGAGCGAGACCCCAACTCTATTCAAAAAAATTTTTTAAGTTTAAATAGAATTA
-----+-----+-----+-----+-----+-----+

      23230              23250              23270
      .               .               .
TATAAAAAAGGAAAAGAAAAATGCTGTTTCATAGCGTTCCTAGTTTAGCATGGGAGAGAC
-----+-----+-----+-----+-----+-----+

      23290              23310              23330
      .               .               .
CAGGTCTCCCTGGGTGGTTGTCTGTGTGTGTGCTGGGTGTGCGTGGCAGGGCTAGTGTGT
-----+-----+-----+-----+-----+-----+
```

FIG. 29

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23350	23370	23390
GGGGTCCGTCTAGGCACATTCAGGCGCCGAATCCCGTGGCTCCCAGGTTTACCTGACGGT		
-----+-----+-----+-----+-----+-----+		
23410	23430	23450
GCAGCCTGGGGTGGAGACTTAATGAGGGCGGGGAGTTGCTGCAGCAAAGGCTCCTCCCAG		
-----+-----+-----+-----+-----+-----+		
23470	23490	23510
GGGTATCAGCGCAGACAGCTGGGTTTTCACTGTGCTCCTGCTCCAGAGGCACTAGGAAGG		
-----+-----+-----+-----+-----+-----+		
23530	23550	23570
GGGCGCCTATCAGACTAGGACTCTGCCAGCCATCCTTCTCTGTTGAAGGTCCAGC		
-----+-----+-----+-----+-----+-----+		

FIG. 29

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```

      10              30              50
CAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTGCTGCTGCTGCTACTAC
-----+-----+-----+-----+
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuLeuL

      70              90              110
TGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGCAGC
-----+-----+-----+-----+
euLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnP

      130             150             170
CAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGC
-----+-----+-----+-----+
roValThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluP

      190             210             230
CGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGC
-----+-----+-----+-----+
roValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuLeuL

      250             270             290
TTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCC
-----+-----+-----+-----+
euGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHisTyrGlyP

      310             330             350
CAGATGGGCAGCCAGTGGTCTGGCCCCCAACCACACGGATCATTGCCACTACCAAGGGC
-----+-----+-----+-----+
roAspGlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyA

      370             390             410
GAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCC
-----+-----+-----+-----+
rgValArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyL

      430             450             470
TGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCA
-----+-----+-----+-----+
euIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerL

```

FIG. 30

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```

      490              510              530
AGGACTTCTCAACCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCT
-----+-----+-----+-----+-----+-----+-----+
ysAspPheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrC

      550              570              590
GTGGCCACAGGGATCCTGGGAACAAAGCGGGCATGACCAGCCTTCCTGGTGGTCCCCAGA
-----+-----+-----+-----+-----+-----+-----+
ysGlyHisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlns

      610              630              650
GCAGGGGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGGAAGTGTACATTGTGGCAG
-----+-----+-----+-----+-----+-----+-----+
erArgGlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaA

      670              690              710
ACCACACCCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAACAGCGTCTCCTGG
-----+-----+-----+-----+-----+-----+-----+
spHisThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuG

      730              750              770
AAGTCGCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTTCAGGTGGCGCTGACCG
-----+-----+-----+-----+-----+-----+-----+
luValAlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrL

      790              810              830
GCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGC
-----+-----+-----+-----+-----+-----+-----+
lyLeuGluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrL

      850              870              890
TCTGGGCCTTCCTGCAGTGGCGCCGGGGGCTGTGGGCGCAGCGGCCCCACGACTCCGCGC
-----+-----+-----+-----+-----+-----+-----+
euTrpAlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaG

      910              930              950
AGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCCTGGCGCCCGTCGAGGGCA
-----+-----+-----+-----+-----+-----+-----+
lnLeuLeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyM

```

FIG. 30

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```

      970              990              1010
TGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCATCGGCG
-----+-----+-----+-----+-----+-----+
etCysArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyA

      1030              1050              1070
CCGCAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACG
-----+-----+-----+-----+-----+-----+
laAlaAlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspG

      1090              1110              1130
GCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGC
-----+-----+-----+-----+-----+-----+
lyCysCysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyH

      1150              1170              1190
ACCCGTTTCCGCGCGTGTTTCAAGCGCTGCAGCCGCCGCCAGCTGCGCGCCTTCTTCCGCA
-----+-----+-----+-----+-----+-----+
isProPheProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgL

      1210              1230              1250
AGGGGGGCGGCGCTTGCTCTCCAATGCCCGGACCCCGGACTCCCGGTGCCGCCGCGCGC
-----+-----+-----+-----+-----+-----+
ysGlyGlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaL

      1270              1290              1310
TCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGT
-----+-----+-----+-----+-----+-----+
euCysGlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluC

      1330              1350              1370
GCCGCGACCTCTGCTGCTTTGCTCACAACCTGCTCGCTGCGCCCGGGGGCCAGTGCGCCC
-----+-----+-----+-----+-----+-----+
ysArgAspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaH

      1390              1410              1430
ACGGGGACTGCTGCGTGCGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCA
-----+-----+-----+-----+-----+-----+
isGlyAspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaM

      1450              1470              1490

```

FIG. 30

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TGGGTGACTGTGACCTCCCTGAGTTTTGCACGGGCACCTCCTCCCACTGTCCCCCAGACG
-----+-----+-----+-----+-----+-----+
etGlyAspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspV

1510 1530 1550

TTTACCTACTGGACGGCTCACCTGTGCCAGGGGCAGTGGCTACTGCTGGGATGGCGCAT
-----+-----+-----+-----+-----+-----+
alTyrLeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaC

1570 1590 1610

GTCCCACGCTGGAGCAGCAGTGTGCCAGCAGCTCTGGGGGCCTGGCTCCCACTCCAGCTCCCG
-----+-----+-----+-----+-----+-----+
ysProThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProG

1630 1650 1670

AGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACA
-----+-----+-----+-----+-----+-----+
luAlaCysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspS

1690 1710 1730

GCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCC
-----+-----+-----+-----+-----+-----+
erGluGlyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysG

1750 1770 1790

AGGGTGGAAAGCCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACC
-----+-----+-----+-----+-----+-----+
lnGlyGlyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisL

1810 1830 1850

TAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCAGCTGGACC
-----+-----+-----+-----+-----+-----+
euAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspL

1870 1890 1910

TGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGA
-----+-----+-----+-----+-----+-----+
euLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnS

1930 1950 1970

FIG. 30

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GCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACA
-----+-----+-----+-----+-----+
erArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisS

1990 2010 2030
GCCACGGGGTTTGC AATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCT
-----+-----+-----+-----+-----+
erHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProP

2050 2070 2090
TCTGTGACAAGCCAGGCTTGTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACC
-----+-----+-----+-----+-----+
heCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnH

2110 2130 2150
ATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGGGGCCCG
-----+-----+-----+-----+-----+
isAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaG

2170 2190 2210
GCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCT
-----+-----+-----+-----+-----+
lyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyC

2230 2250 2270
GCAGAAGGGACCCTGCGTGTCAGTGGCCCCAAAGATGGCCCCACACAGGGACCACCCCTGG
-----+-----+-----+-----+-----+
ysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuG

2290 2310 2330
GCGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGACC
-----+-----+-----+-----+-----+
lyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspP

2350 2370 2390
CTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTG
-----+-----+-----+-----+-----+
roGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProA

2410 2430 2450
ACCCCCAAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAA
-----+-----+-----+-----+-----+

FIG. 30

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```
-----+-----+-----+-----+-----+-----+
spProGlnAspGlnValGlnMetProArgSerCysLeuTrpEnd

      2470              2490              2510
      .               .               .
TGAACAGATTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAACTGCAGGGG
-----+-----+-----+-----+-----+-----+

      2530              2550              2570
      .               .               .
CAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAAGTTTCTTCCCCG
-----+-----+-----+-----+-----+-----+

      2590              2610              2630
      .               .               .
AGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTGAGGGC
-----+-----+-----+-----+-----+-----+

      2650              2670              2690
      .               .               .
TGGAGAACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGG
-----+-----+-----+-----+-----+-----+

      2710              2730              2750
      .               .               .
TCACACAGCCCCTGACCTCCCTCACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAAG
-----+-----+-----+-----+-----+-----+

      2770              2790              2810
      .               .               .
GGCTCTGTCTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCAGCTCTGT
-----+-----+-----+-----+-----+-----+

      2830              2850              2870
      .               .               .
GGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCCTGGGGCCCTATGGTTCGACTGAGTC
-----+-----+-----+-----+-----+-----+

      2890              2910              2930
      .               .               .
CACACTCCCCTGAGCCTGGCTGGCCTCTGCAAAACAAACATAATTTGGGGACCTTCCTT
-----+-----+-----+-----+-----+-----+

      2950              2970              2990
      .               .               .
CCTGTTTCTTCCCACCCTGTCTTCTCCCCTAGGTGGTTCCTGAGCCCCACCCCCAATCC
-----+-----+-----+-----+-----+-----+
```

FIG. 30

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```

3010          3030          3050
CAGTGTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTG
-----+-----+-----+-----+-----+-----+-----+

3070          3090          3110
TGTCGGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAG
-----+-----+-----+-----+-----+-----+-----+

3130          3150          3170
ACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCCGGG
-----+-----+-----+-----+-----+-----+-----+

3190          3210          3230
GTAGGAGGATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACC
-----+-----+-----+-----+-----+-----+-----+

3250          3270          3290
GCATCTACAGAAAAATTTTAAATTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGC
-----+-----+-----+-----+-----+-----+-----+

3310          3330          3350
TGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTCAACACTGCAGTGAGCTA
-----+-----+-----+-----+-----+-----+-----+

3370          3390          3410
TGGTGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAAATAAAT
-----+-----+-----+-----+-----+-----+-----+

3430          3450          3470
TTTAAAAAGACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

3490
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

```

FIG. 30

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10 30 50
CGGGCACGGGTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG

70 90 110
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGCCCCGGAGAGCTCGGGGGACCCCGTTGC
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

130 150 170
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGAC
euLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

190 210 230
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCCTGGATGGACAACCCTGGCGCACCG
isIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThrV

250 270 290
TCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAG
alSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluG

310 330
GCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGC
lyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArg

FIG. 31

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```
      10              30              50
      .              .              .
CGGGCACGGGTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG
      .              .              .

      70              90              110
      .              .              .
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTGC
      MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

      130              150              170
      .              .              .
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGAC
      euLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

      190              210
      .              .
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCCTGGATGGAC
      isIleProGlyGlnProValThrProHisTrpValLeuAspGly
```

FIG. 32

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```

      10              30              50
GCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCC
      MetGlyTrpArgProArgArgAlaArgGlyThrP

      70              90              110
CGTTGCTGCTGCTGCTACTACTGCTGCTGCTGCTGGCCAGTGCCAGGCGCCGGGGTGCTTC
      roLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuG

      130             150             170
AAGGACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGCTCTGGATGGACAACCCTGGC
      lnGlyHisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpA

      190             210             230
GCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGG
      rgThrValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluA

      250             270             290
CTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGAT
      laGluGlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyT

      310             330             350
ACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGG
      yrIleGluThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrV

      370             390             410
TGAGATGCTTCCATGGGCTCTGGGATGCACCGCCAGAGGATCATTGCCACTACCAAGGGC
      alArgCysPheHisGlyLeuTrpAspAlaProProGluAspHisCysHisTyrGlnGlyA

      430             450             470
GAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCC
      rgValArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyL

      490             510             530
TGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCA
      euIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerL

      550
AGGACTTCTCAACCCACGAGAT
      ysAspPheSerThrHisGlu

```

FIG. 33

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10 30 50
GAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGTTG
MetGlyTrpArgProArgArgAlaArgGlyThrProLeu

70 90 110
CTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGA
LeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGly

130 150 170
CATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTTGATGGACAACCCTGGCGCACC
HisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThr

190 210 230
GTCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAA
ValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGlu

250 270 290
GGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCATGGCCTGATCACCTCAGCAGGAAT
GlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisGlyLeuIleThrLeuSerArgAsn

310 330 350
GCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCCACGAG
AlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThrHisGlu

AT

FIG. 34

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10 30 50
GAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCCGGAGAGCTCGGGGGACCCCGTTG
MetGlyTrpArgProArgArgAlaArgGlyThrProLeu

70 90 110
CTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGA
LeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGly

130 150 170
CATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACC
HisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThr

190 210 230
GTCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAA
ValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGlu

250 270 290
GGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATACATA
GlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIle

310 330 350
GAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGATCAT
GluThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrAspHis

370 390 410
TGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGC
CysHisTyrGlnGlyArgValArgGlyPheProAspSerTrpValValLeuCysThrCys

430 450 470
TCTGGGATGAGTGGCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGG
SerGlyMetSerGlyLeuIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrp

490 510
CCACCCCGGGGCTCCAAGGACTTCTCAACCCACGAGAT
ProProArgGlySerLysAspPheSerThrHisGlu

FIG. 35

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10 30 50
CTGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCC
LeuAlaProGlyTyrIleGluThrHisTyrGlyProAspGlyGlnProValValLeuAla

70 90 110
CCCAACCACACGGATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGG
ProAsnHisThrAspHisCysHisTyrGlnGlyArgValArgGlyPheProAspSerTrp

130 150 170
GTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCACCTCAGCAGGAATGCCAGC
ValValLeuCysThrCysSerGlyMetSerGlyLeuIleThrLeuSerArgAsnAlaSer

190 210 230
TATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAACCCACGAGATCTTT
TyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThrHisGluIlePhe

250 270 290
CGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAA
ArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyHisArgAspProGlyAsnLys

310 330 350
GCGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCAGGCGAAAAGCGCGCAGG
AlaGlyMetThrSerLeuProGlyGlyProGlnSerArgGlyArgArgLysAlaArgArg
Glu

370 390 410
ACCCGGAAGTACCTGGAAGTGTACATTGTGGCAGACCACACCCTGTTCTTGAAGTCCGGCAC
ThrArgLysTyrLeuGluLeuTyrIleValAlaAspHisThrLeuPheLeuThrArgHis

430 450 470
CGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAGTCGCCAACTACGTGGACCAGCTT
ArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValAlaAsnTyrValAspGlnLeu

490
CTCAGGACTCTGGACATTTCAGGTGGC
LeuArgThrLeuAspIleGlnVal

FIG. 36

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      10              30              50
      .              .              .
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
      .              .              .
GGGGCCTGGCTCCCACCCAGCTCCCGAGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

      130             150             170
      .              .              .
TGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

      190             210             230
      .              .              .
TGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

      250             270             290
      .              .              .
GGTGCCAGTGGACTCTACCGTTACCTAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

      310             330             350
      .              .              .
GGCACTCCCCAGTGCCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

      370             390             410
      .              .              .
GTGTGGACCTAGAATGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGC
nCysGlyProArgMetValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAl

      430             450             470
      .              .              .
TCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGC
aProProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAl

      490
      .
TGAAAACCATGACACCTTCCTGC
aGluAsnHisAspThrPheLeu

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FIG. 37

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      10              30              50
      .              .              .
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
      .              .              .
GGGGCCTGGCTCCCACCCAGCTCCCAGGGCTGTTTCCAGGTGGTGAACCTCTGCGGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

      130             150             170
      .              .              .
TGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

      190             210             230
      .              .              .
TGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

      250             270             290
      .              .              .
GGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAAGTGACTGTGCGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

      310             330             350
      .              .              .
GGCACTCCCCAGTGGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

      370             390             410
      .              .              .
GTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCT
nCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPheGlnGluLe

      430             450             470
      .              .              .
TCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCA
uGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHisAsnCysHi

      490             510             530
      .              .              .
CTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTGGTGGCAGCATGGA
sCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlyGlySerMetAs

      550             570
      .              .
CAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGC
pSerGlyProValGlnAlaGluAsnHisAspThrPheLeu

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FIG. 38

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      10              30              50
      .              .              .
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
      .              .              .
GGGGCCTGATGGCCAGGAAGTGACTTGTCGGGGAGCCTTGGCACTCCCCAGTGCCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

      130             150             170
      .              .              .
GGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

      190             210             230
      .              .              .
CCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

      250             270             290
      .              .              .
CCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

      310             330             350
      .              .              .
ACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

      370
      .
AAACCATGACACCTTCCTGC
uAsnHisAspThrPheLeu

```

FIG. 39

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10 30 50
GGCCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTGGGGCTGCAG
AlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysAr

70 90 110
AAGGGACCCTGCGTGAGTGGCCCCAAAGATGGCCCACACAGGGACCACCCCTGGGCGG
gArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGl

130 150 170
CGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGACCCTGA
yValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspProGl

190 210 230
GAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCC
uAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProAspPr

250 270 290
CCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCCTAAAAT
oGlnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

310
GAACAGATTTAAAGACAGGTGGCC

FIG. 40

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      10              30              50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCAGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
GGGGCCTGATGGCCAGGAAGTGACTTGTGGGGAGCCTTGGCACTCCCCAGTGCCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

      130             150             170
GGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

      190             210             230
CCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

      250             270             290
CCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

      310             330             350
ACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

      370             390             410
AAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGG
uAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGl

      430             450             470
GGCCGGCCTGGCCTGGTGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTG
yAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTr

      490             510             530
GGGCTGCAGAAAGGACCCCTGCGTGCACTGGCCCCAAAGATGGCCACACAGGGACCACCC
pGlyCysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisPr

      550             570             590
CCTGGGCGGCGTTACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCT
oLeuGlyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLe

      610             630             650
GGACCCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTC
uAspProGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSe

      670             690             710
GCCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGC
rProAspProGlnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

      730             750
TCCTAAAATGAACAGATTTAAAGACAGGTGGCC

```

FIG. 41

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      10              30              50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

      70              90              110
GGGGCCTGGCTCCCACCCAGCTCCCGAGGCCTGTTTCCAGGTGGTGAACCTGCGGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

      130             150             170
TGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

      190             210             230
TGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

      250             270             290
GGTGCCAGTGGA CTCTACCGTTCACCTAGATGGCCAGGAAGTGACTTGTCGGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

      310             330             350
GGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

      370             390             410
GTGTGGACCTAGAATGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCT
nCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPheGlnGluLe

      430             450             470
TCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCA
uGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHisAsnCysHi

      490             510             530
CTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGA
sCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlyGlySerMetAs

      550             570             590
CAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGT
pSerGlyProValGlnAlaGluAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerVa

      610             630             650
CCTGCTGCCTCTGCTCCCAGGGGCCGGCCTGGCCTGGTGTGCTACCGACTCCAGGAGC
lLeuLeuProLeuLeuProGlyAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAl

      670             690             710

```

FIG. 42

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CCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGA
aHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSerGlyProLysAs

730 750 770

TGGCCACACAGGGACCACCCCCTGGGCGGCGTTCACCCCATGGAGTTGGGCCCCACAGC
pGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeuGlyProThrAl

790 810 830

CACTGGACAGCCCTGGCCCCCTGGACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGA
aThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSerSerHisProGl

850 870 890

GAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGATCAAGTCCAGATGCCAAGATCCTG
uLysProLeuProAlaValSerProAspProGlnAspGlnValGlnMetProArgSerCy

910 930 950

CCTCTGGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGC
sLeuTrpEnd

970 990 1010

CACTCCAGGAACCTTGAAGTGCAGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTG

1030 1050 1070

CAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCA

1090 1110 1130

GAGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGGCACACTCTCCAGCTCAA

1150

TAAACCATCAGTCC

rt772

FIG. 42

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10 30 50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110
GGGGCCTGATGGCCAGGAAGTGACTTGTCTGGGGAGCCTTGGCACTCCCCAGTGCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

130 150 170
GGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

190 210 230
CCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

250 270 290
CCACAGCCACGGGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

310 330 350
ACCCTTCTGTGACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

370 390 410
AAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGG
uAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGl

430 450 470
GGCCGGCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGCTG
yAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTr

490 510 530
GGGCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACCACCC
pGlyCysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisPr

550 570 590

FIG. 43

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CCTGGGCGGGCGTTCACCCCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCCCT
oLeuGlyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLe

610

630

650

GGACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTC
uAspProGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSe

670

690

710

GCCTGACCCCCAAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCC
rProAspProGlnAspGlnValGlnMetProArgSerCysLeuTrpEnd

730

750

770

TAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTTGAACCTGC

790

810

830

AGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAGTTTCTT

850

870

890

CCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCTG

910

930

950

AGGGCTGGAGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCC

FIG. 43